

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Gatanaga, T.
Granger, G.A.
- (ii) TITLE OF INVENTION: Factors Altering Tumor Necrosis
Factor Receptor Releasing Enzyme Activity
- (iii) NUMBER OF SEQUENCES: 154
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: MORRISON & FOERSTER
(B) STREET: 755 PAGE MILL ROAD
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94304-1018
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: Windows
(D) SOFTWARE: FastSEQ for Windows Version 2.0b
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: USSN 09/081,385
(B) FILING DATE: 014-NOV-1998
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME:
(B) REGISTRATION NUMBER:
(C) REFERENCE/DOCKET NUMBER: 22000-20577.21
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 650-813-5600
(B) TELEFAX: 650-494-0792
(C) TELEX: 706141

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4047 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AAGCTTTT	CTTCTTCC	CCGGAAAGG	CCGGGGCCAG	AGACCCGCAC	TCGGACCAGG	60
CGGGGGCTGC	GGGGCCAGAG	TGGGCTGGGG	AGGGCTGGGA	GGGCGTCTGG	GGCCGGCTCC	120
TCCAGGCTGG	GGGCCGCCAG	CTCCGGGAAG	GCAGTCCTGG	CCTGCGGATG	GGGCCGGCGG	180
TGGGGCCCGG	CGGGGCGGCC	TCGGGAGGCG	TCCAGGCTGC	GGGAGCGGGA	GGAGCGGCCG	240
TGCGGGCGCC	AGCGCCGTGG	GTGGAGGTGG	CCGTCCCTCC	TGAGGGGCAG	CCAGTGCGTT	300
TGGGACCCGG	GAGCAGAGCC	CGCGCCTCCC	CAGCGGCCCTC	CCCGGGGGTC	TCACCGGGTC	360
ACCCGAGAGC	GGAGGCCCGG	GCTCCGCAGA	AACCCGGGGC	GGCCGCGGGG	AAGCAGCGCC	420
CTCAGGCGTC	GGAGGAGCCC	CCAGAAGGAC	CTCGCGCCTT	CCCGCCGGGC	TCCGACCGCC	480
TGGGTTCGGT	GCGGGACGGC	CCAGGCCGCC	AGGACCCCCA	AGCGCAGCTC	AGTCTGCGGG	540
GCACGACCCA	GAGGCCAGCA	GCAGAGGACG	GGGCCGGGGC	CGGGAGAGGG	CGGGGAGGGC	600
GCTCCTGGGA	GGTCAAGGCC	AGGGCTAGAC	TTTCAGGGTC	ATGGCCTGGC	CCCTCATCCC	660
CAGGGAGGTG	AGGGGGCTCT	GTGAGCAGAG	GGGGCCCCGG	TGGAGAAGGC	GCTGCTAGCC	720

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AGGGGCGGGG CAGGAGCCCA GGTGGGGACT TAAGGGTGGC TGAAGGGACC CTCAGGCTGC 780
AGGGATAGGG AGGGAAGCTA GGGGTGTGGC TTGGGGAGGT GCTGGGGGAC CGCGGGCGCC 840
CTTTATTCTG AAGCCGAATG TGCTGCCGGA GTCCCCAGTG ACCTAGAAAT CCATTTCAAG 900
ATTTTCAGGA GTTTCAGGTG GAGACAAAGG CCAGGCCAG GTGAAAATGT GGCAGTGACA 960
GAGTATGGGG TGAGAACCAC GGAGAGAGGA AGTCCCCGAG CGGGATGATG GGACAGAGAG 1020
CGGGGACCAG AATTTTTTAA AACGCATCTG AGATCGGTTT GGCAGACTCA TAGTTGTTTT 1080
CCTTTCACGG AGAAAGTGTG GGCAGAAGCC AGCTCTAAAG CCCAGGCTGC CCAGCCTGCA 1140
CTGGCAGAGC TGACGGAAGG CCAGGGCAGA GCCTTCCCTC CCGTGCACAG ACATGAGCCC 1200
TGGAGATCTG GAATGAGGCA GATGTGCCCA GGGAAAGCTG ATCCGCCCGG ACCCAGGGCC 1260
CCCCGGGTGC CCCTTTGAGC GTGGAATCGT TGCCAGGTCA TGGCTCCCTG CTATCGAACA 1320
CCGGACACGG GTCGTGTGCT GCACCTGGCA GTTGCAGGAC CGACACCCAC AATGCCTTAA 1380
GAGGTGATGA CTGCCTTCCA GGGGCTTGGC TGGCTGACAC TTTGCATGGC TCCTGGAGAA 1440
GAGGGATTGA GTGGAGTCCA CGGGTCATGG CCACGTCCTG GGTGCTGCCT CTGAGGCAGG 1500
GCCCGGCTGG GGTGAGAAGG GGCTGGAGAC AGGTTCTGTC CAGTTCAGCC TCTAACCGGT 1560
GGTCTTTCAT CCTAGGAACC CACTGGGGGC TTATGAAACT GCAGGTGGCT GAGTCCTTGC 1620
CATGGGTCTC CTCCTTCAGG AGGTCTGGGT GGGGCCGGAG ACTGTACCCC ACAAGGGGTC 1680
CCAGGTGAGG CGGATGTGGC CTGGCGCTGT GTGGCTCTGG ACCTAGTCCT TGGGCTTGGG 1740
CTGGCGCCCA GGGCCTGGGC TTGAGACAGC TGTGACGCGA GCAAGCCATT TACCCCGTTT 1800
GTGGGGACAT TACATCTTCC TAGCTTGGAA CACACAGGCA GCCAGGGTTG TTATCCACAT 1860
TCCTCTTCCA TGTCTTCTC TTGAGAACTT TTACCAGGTA TGTCAGGAGC TGGGCTCCAC 1920
CAGGGAGACT CAAGTGGAAA GCCCTCATCC TTGTCTTCCA GGAGACAGGA AAACCTATGG 1980
TTACAATTCC AGGGACAAGA GCGATGCATG TGAGGTGTGG CAAATCTCAC GTTCAACTG 2040
GAGAAATCAG AGACAGCTTC CTGGAGGCGA TGACACCTGG ACAGGCTTCT CCACAGGAGG 2100
AAGCGAGTGA GAGAAGCCAA CYGGGATGGA CCCATCATGT AGGGGGAACA GTGCGCGCAG 2160
AACCAACAAC CACCCCAACC CTAGGCCAG AGCTCACGGA GAGAGCTGGG CCTCTCGGGG 2220
TGACTACATA GTTCCCTGCT GGATCTTAGG TCTTGTCTT GGGCAGCTCT GCTGAGACCT 2280
CTATGCCTGT TCCAGGCTGC ACCAAGGTTT TGTGACTATT GGTCTGGGGT TGTTTTGCAG 2340
CAACTGAAAG GTTCTGTTGT AAAACAGGCA CTTGATTTGC TGGAAAGGAAT GCTGTTTGT 2400
CTTGCTGCGA CAAACATTGA GCAGCATTTA GTGGGCGGTT TATATCTTGT GGAGTAATGG 2460
GTGTTTTTGA AGTCTGTCTT GGGTACTGCA CATTAAAGG AATATCATTT TCTGAAACAT 2520
TGCTATTTTC CACACCAGAA ATCATATCCT CTTGCTGGTC CATGCTGTA GACCTTACAC 2580
GAGAAAGTCT TAATGTAAGT TTAGTAGAGT CCTTGGATGG AGAACTAATT ATATCATACA 2640
TTGCCGCTTT CTCACCTCTG TCTTTTTCAT CCTTGCTTAA TTTCATTTTT TCTGCTTCT 2700
TTTGTTTTCT TTCTGGAGAA TCTAGCAAGA TATCTGGTGG AACATCTCGA GGTGATGAAC 2760
AAGGTAGAGA CTGAGATTGT AGGATTAAAG GTGGTCTTGA GCCTTTAGGA GTTCTTTCAC 2820
TTCCAGCAGG GGAGCATACT GGCTGTGGAG ATCTCAAGGG AAAAGATGCA GCATTCCTCA 2880
TTGTGGAAGA ATCTCCATCG TCACTACTTA GCCTGTGCAC CATGTGTAGG TAGTCCTCAC 2940
TTGAACCATG TCTAGGATTA TCAGCATGAT GATTAGCTGA ATTGCCAGAC AACGGACCAG 3000
AAACTTTATT ATCATGTATG TTTCTCAAAC CACCTGCAAC AATGGGACTT GATACCGATG 3060
CTTGTTGTCAT CTGTGGATGT GTTGTGTAAC TTGAAGGATG GGAATATGGC ATGTATCCTG 3120
CAGGGCTTTG TGGGGCGTAT GGACTAGGCA CTGGGCTATT TTGCTGTGGC ATAAATCTGT 3180
TCCCAGAGCT TGTCTGTGGT GGCACAAACC GGCTGGAGGG GCTATGTGAG ATAGTGGTTT 3240
GTTGATAATT GGAAGATGCA GGACTACTGT GCATGGAATT CTGAGAAAGT TTATACTGAG 3300
ACATCATCAT TCCACTTTGT ACATATCTGT TCTGCATGCT TTTCTCCCTG AAAACATTAG 3360
GACTCCTTGC CAGGACGGCC TGCAACAAGA CTGGTATGTC ACCTTCTGGG TCATCACTGC 3420
CAAGGTTATC TTTCAACTCT ATGTGATCTG TTGATACCTG GTTGAGGCTA TGGACAAGCT 3480
GTGAAACCAA ATTGTCATCC CTACAAGCCA AAAGGCAGTT CACCTCTTCT GCTATTCGTG 3540
CATTAAGAGG AAGGCTCTTT GTAGTTGTAG CAGGYAAAGG AGATGGAAGA GGCAGCTGGT 3600
TCAGGAGGTC TGTGAGACTA GCAATCCCCG CAAGAGTAGT AATGGGGACA TGGGGCATAT 3660
CCCCATTCTT CCTGAATTTT TGGAAATGGT TTGCCTATAA AAGTACTTAG TTCAGGTGCC 3720
AGCTGTCTAT ACTTCCCAT TCCCAACAC TGGGCGAATC GGCCTCTGAA TCCAAGGGGA 3780
GGCCGAGGCC GCTGTGGCGA GAGACTATAA TCCGGGCCGG GAGGGGGGGC GGCTACGGCT 3840
CCTCTTCCGT CTCCTCAGTG CGGGGAACAT GTAGAGCCGG GGGGAGACCA GCCGAGAAGA 3900
CAAATCGTTG CTTCTTCTTC CTCCTCTTCC TCCTTCTCCC ACATAGAAAC ACTCACAAC 3960
ACCCGACCAC GGGCCCGAGC TACCGGGGGG GCATCGCCGC GGGCCCGGGA ACCAATTCTC 4020
CTGTGCGCGG GGGCGTCTT TGGATCC 4047

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 739 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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GGATCCAAAG GTCAAATCC CCACCTGGCA CTGTCCCCGG AGCGGGTGGC GCGGGGCCGG 60
CCCGGGCGCG GCGGCTTGGC GCCAGAAGCG AGAGCCCTC GGGGCTCGCC CCCCCGCTC 120
ACCGGGTCAG TGAAAAAACC ATCAGAGTAG TGGTATTTCA CCGGGCGGCC GCAGGGCCGG 180
CGGACCCCGC CCGGGGCCCC TCAGGGGGAC ACCGGGGGGG CGCGGGGGG CTCCCACTTA 240

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TTCTACACCT	CTCATGTCTC	TTCACCGTGC	CAGACTAGAG	TCAAGCTCAA	CAGGGTCTTC	300
TTTCCCGCT	GATTCCGCCA	AGCCCGTTCC	CTTGGCTGTG	GTTTCGCTGG	ATAGTAGGTA	360
GGGACAGTGG	GAATCTCGTT	CATCCATTCA	TGCGCGTCAC	TAATTAGATG	ACGAGGCATT	420
TGGCTACCTT	AAGAGAGTCA	TAGTTACTCC	CGCCGTTTAC	CCGCGCTTCA	TTGAATTTCT	480
TCACITTTGAC	ATTCAGAGCA	CTGGGCAGAA	ATCACATCGC	GTCAACACCC	GCCGCGGGCC	540
TTGCGGATGC	TTTGTITTA	TAAACAGTC	GGATTCCCT	GGTCCGCACC	AGTTCTAAGT	600
CGGCTGCTAG	GCGCCGGCCG	AAGCGAGGCG	CCGCGCGGAA	CCGCGGCCCC	CGGGCGGGAC	660
CCGCGGGGGG	GACCGGGCCG	CGGCCCTCC	GCCGCTGCC	GCCGCCCGCG	CCGCCGCGCG	720
CCGAAGAAGA	AGGGGGA					739

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CAAGAGTGGC	GGCCGCAGCA	GGCCCCCGG	GTGCCCGGGC	CCCCCTCAG	GGGGACAGTG	60
CCCCCGCGC	GGGGGCCCG	CGGCGGGCCG	CCGCCGGCCC	CTGCCGCCCC	GACCTTCTC	120
CCCCCGCGC	CGCCCCACG	CGGCGCTCC	CCGGGGAGGG	GGGAGGACGG	GGAGCGGGG	180
AGAGAGAGG	AGAGAGAGG	CGCGGGTGG	CTCGTGCCGA	ATTCAAAAG	CTT	233

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2998 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGATCCAAAG	AATTCGGCAC	GAGGTAGTCA	CGGCTCTGT	CATTGTTGTA	CTTGACGTTG	60
AGGCTGGTGA	GCTTGGAAAA	GTGATGCGC	AGCGTGACG	AGGCGTTGTA	GATGTTCTGC	120
CCGTCCAGCG	ACAGCTTGGC	GTGCTGGGCG	CTCACGGGGT	CCGCATCTG	CAGCAGGGCC	180
TGGAACCTGGT	TGTTCTTGGT	GAAGGTGATG	ATCTTCAACA	CTGTGCCGAA	CTTGAGAGAA	240
ATCTGGTGCA	GCACATCCAG	GGTCACAGGG	TAGAAGAGGT	TCTCCACGAT	GATCCTGAGC	300
ACGGGGCTCT	GCCCGGCCAT	CGCCATCCCT	GCATCCACGG	CCGCCGCCGA	GGCAGCCAAG	360
GCCAGGTTCC	CCGACTGGAC	CGAGTTTACC	GCCTGCAGGG	CCGCTGGGG	CCGCGCCTGG	420
TTGGGAGAGC	TGTCGGTCTT	CAGCTCCTTG	TGGTTGGAGA	ACTGGATGTA	GATGGGCTGG	480
CCGCGCAGCA	CAGGGGTCAC	CGAGGTGTAG	TAGTTCACCA	TGGTATTGGC	AGCCTCCTCC	540
GTGTTTCATCT	CGATGAAGGC	CTGGTTTTTC	CCCTTCAGCA	TCAGGAGGTT	GGTGACCTTC	600
GCAAAGGGCA	GCCCCAGGGA	GATGACTTCC	CCCTCCGTGA	CGTCGATGGG	GAGCTTCCGG	660
ATGTGGATCA	CTCTAGAGGG	GACGCTGCA	CTTCGGCTGT	CACCTTTGAA	CTTCTTGCTG	720
TCATTTCCGT	TTGCTGCAGA	AGCCGAGTTG	CTGCTCATGA	TAAACGGTCC	GTTAGTGACA	780
CAAGTAGAGA	AAAGCTCGTC	AGATCCCCGC	TTGTACCAA	CGGCTATATC	TGGGACAATG	840
CCGTCCATGG	CACACAGAGC	AGACCCGCGG	GGGACGGAGT	GGAGGCCCGG	GAATCCTGGA	900
GCTAGAGCTG	CAGATTGAGT	TGCTGCGTGA	GACGAAGCGC	AAGTATGAGA	GTGTCCTGCA	960
GCTGGGCCGG	GCACTGACAG	CCCACCTCTA	CAGCCTGCTG	CAGACCCAGC	ATGCACTGGG	1020
TGATGCCTTT	GCTGACCTCA	GCCAGAAGTC	CCCAGAGCTT	CAGGAGGAAT	TTGGCTACAA	1080
TGCAGAGACA	CAGAAACTAC	TATGCAAGAA	TGGGAAACG	CTGCTAGGAG	CCGTGAACCT	1140
CTTTGTCTCT	AGCATCAACA	CATTGGTCAC	CAAGACCATG	GAAGACACGC	TCATGACTGT	1200
GAAACAGTAT	GAGGCTGCCA	GGCTGGAATA	TGATGCCATC	CGAACAGACT	TAGAGGAGCT	1260
GAGTCTAGGC	CCCCGGGATG	CAGGGACACG	TGGTGCAGTT	GAGAGTGCCC	AGGCCACTTT	1320
CCAGGCCCCAT	CGGGACAAGT	ATGAGAAGCT	GCGGGGAGAT	GTGGCCATCA	AGCTCAAGTT	1380
CCTGGAAGAA	AACAAGATCA	AGGTGATGCA	CAAGCAGCTG	CTGCTCTTCC	ACAATGCTGT	1440
GTCCGCCTAC	TTTGCTGGGA	ACCAGAAACA	GCTGGAGCAG	ACCCTGCAGC	AGTTCAACAT	1500
CAAGCTGCGG	CCTCCAGGAG	CTGAGAAACC	CTCCTGGCTA	GAGGAGCAGT	GAGCTGCTCC	1560
CAGCCCAACT	TGGCTATCAA	GAAAGACATT	GGGAAGGGCA	GCCCCAGGGT	GTGGGAGATT	1620
GGACATGGTA	CATCCTTTGT	CACCTTGCCT	CTGGCTTGGG	CTCCTTTTTC	TGGCTGGGGC	1680
CTGACACCCAG	TTTTGCCAC	ATTGCTATGG	TGGGAAGAGG	GCCTGGAGGC	CCAGAAGTTG	1740
CTGCCCTGTC	TATCTTCTG	GCCACAGGGC	TTCAATCCCA	GATCTTTTTC	TTCCACTTCA	1800
CAGCCAAACGG	CTATGACAAA	ACCACTCCCT	GGCCAATGGC	ATCACTCTTC	AGGCTGGGGT	1860
GTGCTCCCTG	ACCAATGACA	GAGCCTGAAA	ATGCCCTGTC	AGCCAATGGC	AGCTCTTCTC	1920
GGACTCCCTT	GGGCCAATGA	TGTTGCGTCT	AATACCCTTT	GTCTCTCTC	TATGCGTGCC	1980
CATTGCAGAG	AAGGGGACTG	GGACCAAGG	GGTGGGGATA	ATGGGGAGCC	CCATTGCTGG	2040

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CCTTGCATCT GAATAGGCCT ACCCTCACCA TTTATTCAC TATACATTTT ATTTGTGTTT 2100
TCTAATTTAA AATTACCTTT TCATCTTGCT TGATTTTCCT TCAGCTAAAT TAGAAATTTG 2160
TAGTTTTTCC CTAATAAAAT TCAATGGCAT TCTTTCTTAT AAATTACAT CTCTGATTTT 2220
CTTGTCAGCC TGCTTCAAGG AAATCCATGT GTTCAAAATG CTTGCTCGCA GTTTGCTCCA 2280
TACCAAATGG TTGCTTAACC CAAATATCTG AGCAGCAAAAT TGAGCTGATC CTCTGGGAGA 2340
AAGTACGGTT GAACAGCCAA GACCACTGGG TAGTCGAAGA GAAGACCACA CATCCTGAAC 2400
TCCCCAGTCT GGTGTGAGGG GAGGACAGCT GATAACTGGA TATGCAGTGT TCCCAGACAT 2460
CACTGGTCCC AAACCATTTAC TTCTGCCTGC CACTGCCACA AATACAGTAG GAATGCCATC 2520
CCCTTCATAC TCAGCTTTAA TCCTCAGAGT TTCTCTGGT CCTTTATGCG CAGATGTTAC 2580
TCGAAGTTCA CATGGAATGC CAAAATTTCC ACAGGCCCTT TGTATTTTTT CACAGTGACC 2640
AAGATCAGAA GTAGAGCCCA TCAACACTAC AACCCTGCAC TGACTTTCTG ATTTCAAAG 2700
CAACTCTACT CTCTCTGCAA CCCACTCAAA GTTTTCTTT ACCATTTTGA GCCCTTCAGG 2760
AGTTACTTCT TTGAGGTCCT GATAAGACTG TTTGTCTTTC TGTGTGGCTC GATCTCTGTA 2820
TGGCCAGAGT CTCCAGGAAT CATTGTCAAT AACATCAGCA AGAACAATTT CTTTGGTGGT 2880
TACATCAACA CCAAATTTCAA TCTTCATATC AACCAGTGTA CAATTCTGGG GCAACCAGGA 2940
TTTCTCCAGT ATTTCAAATA TAGCTGTGT AGCATCTCGT GCCGAATTCA AAAAGCTT 2998

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(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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AAGCTTTTTG TGAACACCCT AGGATATGTC CCCTCCCTCA CCACACCCAA CCCCCCGCCC 60
CTGCCCCAGG ACATGACGAT GCCTCACACA CACACATACA CACAAGGCCG 120
TGAGCTGCAC GCAGGAACAT GGGCTGCACT CAGGACAACA TTGAAAAAAT ATACATTATA 180
TATGTACACC CGGGGCCCCC ACGTCCCTC CCGTCCCCGC AGCCTGGCCA CACCAGGTCA 240
CGGAGGAGGG GCGGGGGCTG CAGGACCTCA GGAAGTGAAG GGCAGGAAGG GAAACAGGAC 300
AAGAAAGGAA GGAAGTTGGA AAGGAGGGAG AAATGGGGT CCCAGACTGA AATGGAAATG 360
AGGTGGGGCG ATCATAAGAG AAGCAGGGAC GATGGTCCAG CTGAGGGAGC CCTGCAGAGG 420
GGGAAAGGCT TCCCATGGAC AGGAGAGAGA AGGGAAGGGG AGAGGAGAGG GTTTCCTTCA 480
ATCCCAACCC CAGCCCCAGC CCCAGCCCCA GCCATTGCAA TCGTCACCC CTCCCCAACA 540
CAGTGAGTGC TAAGGGGGCA GCTGCCATTG GGGGTAGAAA GGCAGCTGAA GTCCAGCCCA 600
CTTTCCAACC CAGCCAGCCC CAGTGAAGG GGCACACCAG GAGCATGACA GCCCAGAAGT 660
GAGGGATGGG GGGCCGGGGG AGGGGCAAGG CGGACTCCAG AGGGCCCGCT GGGGTTTTGA 720
AATGAAAGGA GGAAGTGGT TGAAGCCTCT CTCCCTCTTG GTCTCTGTGT TCCAGAAAG 780
TCCTTCTCCC ATGTCTGGAG TGTCTGTTT ACCAGGGCAG AATTCCTTCT CTGCGTGGGG 840
AGAGGTGTAG GCCTTAGTAG CGGTGTGGG GGGTCTCGAT GATGCGTCTC TCGTCTGCTG 900
TGCGGGAATC GGCCACCTCC GAGTCACTGC TGTCTCATC CTCCTGCTGG CCCCCAACAG 960
CCCCCGTCA ACAGGACTGC CGATTCTGGT AGGACTCCAT GGGGTTTACA ATGATGGTGA 1020
GAGCTGAGTC ATCCAGAAG AGGTCTGGGT CCTTGGGGTC ACTGGAGGCC CTGGAGGCC 1080
CGCCGGCCCC TGAGACGCGG CGGTGAAGGG AATGGATGCG CACCAAGGCC AGGACGACCA 1140
TGAGCACCAG GAAGCCACG CACACCACAA TGATGAGGGT TCGGGCGCTG GGTATCATGG 1200
AGTTTCTGTG GGAGCTGGCT AGGCTGTGTC CAGCCATCTC AGGCGGGGGC TGGTGACCAC 1260
GGTGCAAGAA CTGCTGGGAG CTGAGCACGT GGCTGGGGTG GGCAACCCCG TTCTGCTGT 1320
GCAGGACATT GACCTCCACG ATGAATTCAT TGCTGGAGTA ACGGCCATT CATTCCGAGC 1380
AGGAAAGCCG GAACCTTCTG GTGTAGAGGG CAGCTCCGTG TCGCAGCCGA TAACGAGCCT 1440
GCCTCAGGAT CTCTTCATAC ACAGTGATGC TCTCCACCCC AGCAATAGTG AGGTAGGCAG 1500
ATGTGTTGGT GAGCTCCAGC CCCCCTGCT GCAGAGAGGT TGTGTCCAGG AGCAGGCTTT 1560
CCCCCTCGGG ATCCAGGTCA TCCCCACCA GAGAAATTT ACAGCCATCC AGGTTGTGCA 1620
CAATCTCATC CGACATGCGT GTGTCTGTCA CTGTGCCCTG CCAACTCTCA TCCTTTTGG 1680
CCTCCACCTG GTGAGAAATG GAGCAGGTGA TTTGAAGATC AGGGAACAAA GGGACGCCGT 1740
TGGTTCCTTC AAAGTCCACA GCTGGGGGGG CAAATGAGC AGTGCCACTC AGCAGGATCT 1800
GGGGGGGGCT AGGCTGAAGG ACGACCACGT AGCCCTCCAC TTCAGGGATG GAGACGCAGG 1860
ACTCTTCGCT GAAGCACTTG ACAGCAGTGG TGAGGCGCAG GGGCCTGACG CCGGGCGTGG 1920
CAAAGCGCAG AGTGTTCATG TAAGCCACAT GCTGCAGGGC ATGGTTGAAG GTCTCCACAT 1980
CATCCCCCTC CAGGGTGAGC AGGGAAGTGT AGGGGTTTCA GTGGACCTTC ATGCCCTTTC 2040
CCAGGCTCTC GAAATCCCTA TAGTCCAGCC CCTCCCGACA TGATAGAGG CACTCGATGA 2100
CCTCGGGCTC CTCCAGGCGA CCGTGAAGCC AGCCAGGTAG CCATGGAAGT 2160
AGTGGTGGAT CGACAAAGGG TCTCCTTGGG TGGTGTCTGT ACTGTTGTCT CCCTTTTCTT 2220
TCTCTTTGTT CTCTCTCTCA GTCCAGCAGG CCCCAATCAT GAGAGCAGGC TCCCTTCGGG 2280
GTGGGTGGAT GAGGCCATTG TCATGGATGA GGGCAGGGTC GAAGGAGATG CCGTCGGTAT 2340
AGAGTGTGAC TGTGGGGAAC TCGAGGTTC GAGCGTAGTG GTGCCACTCA TCATCACAGA 2400
CCTGCTCCAG CTTCAGAGG AACTTGACTG GCGGGGCACT CTCAGGAGG GGCAGTAGA 2460
GGAAGGCAAT CTAACAGCGG TGGACAGTCA GCGAGTAGTG AGAGAAGCCG TCCTCATCT 2520
GGACAGTGTT ACATACGATG GTTTCCTCTT CCTTCTTGCC CTGTGTTGGA GTTACGCCAT 2580
GCTTCATCCA GAAGGACAGG GTGAAGTGGT CACTGAGGCT GTCTGGGGC CCAGAGCCCA 2640

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GCCCACTGGG	GCCACCCAGG	GGCACCTGCA	CAGCCTGGGT	GCCATTGAAC	CAGTAGATCA	2700
GGCTGCTGTC	CTGGCTGTAG	TGCACCGAGA	GTCTGCTGT	CCAGTTGGCA	TTGGGGCCAG	2760
GCATGGGCAA	CAGATCCACT	TCCCCAGTGG	CAGCACCAACA	GAGTTTCCCG	AGCGCCCGCT	2820
CTGAGTAGTT	GTACCGGTCA	CAGCCCTTGG	CCACATGGCT	GGTCTGCAGC	TCTATGGTGG	2880
CCTGAATGTT	CCAGAGTGGT	TCATCACAGG	TCTCCAGGCG	GATACCAGGG	AACAAAGCCA	2940
AGCTCCCAGC	ACCTGGTGCA	TATTCGATCC	TTTGTGTTCA	GCCTTGCCAG	CTGGGTTTAC	3000
AGGTGGGCTT	CACCTGAATC	TCCACCTCAG	CATCATCTGC	TGCCCCGCTT	TTCCACAGT	3060
CATAAGCTGT	CACTGTAAAC	TTATAGAGCC	TCTCACCAC	GTACTGCAGC	TTCTCTGTGT	3120
TCTCAATGTT	CCCGTCATTG	TCAATGAGGA	AAGGGGTGTT	GGGTGTGAGA	ATCTCATAGT	3180
AGCAGATCTG	GCTGTACTGG	GGGGAGCAGT	CACCGTCAAT	GGCTTCCACC	CGCAGGATGC	3240
GATCGTACAG	CTTCCCCTCT	GTACAGCCG	CACGATACAG	CCGTTCCACA	AACACTGGGG	3300
CAAACCTCGT	CACATCGTTG	ACCCGCACAT	GCACAGTGGC	CTTGTGGGAC	TTCTTGGTGT	3360
TGGCCCCGTC	GGGGCCCTCG	CCACAGTCAT	AGGCCTGGAT	GGTGAAGGTG	TGTTCCCTTCT	3420
GGGCCTCGCA	GTCCACAGGC	TCCTTGGCCC	GGATCAGCCC	CTCTCCTGTC	GCCTTGTCAA	3480
GGATCACAGC	CTCAAAGGGC	ACCCAGAGCC	CATGGAGCCG	GAAGCCGCG	ATCTCACCTG	3540
CATAGCGCAG	CGGGGCATCC	TTGTCCAAGG	CAAAGAGTGG	TGGATTCACT	AGGACCGTGT	3600
TGTCATTCTC	CATGACGATG	CCCTGGTACT	CTGCCTCAAT	GCATGGCTTG	TGCTTGTGG	3660
CTTTGTGTACA	GGAGCAGGAC	GCGAGCAGAG	AGGCCAGCAG	AAGGGGCGAG	AGCAGGAGGG	3720
TCATGGTGGC	GCGTGGGGCA	GGGCAGGGCC	AGGCGTTTGC	CTCCCCTGGG	AGCCTCCAGC	3780
CTGCGGATTG	CACCTTGCGG	GAGGGATACA	GGGGGGGAAA	ACCAAATAA	AACGTCAAAT	3840
AAATTGTGTA	GGAGGAGTCC	AGCTTAGGAC	CGGGCCAGAG	CCAGGCCAGG	CTCGGGGAGG	3900
GGGCCTCTGC	AGGTTTCAGAG	GATCACTGCT	GCCACCACCG	CCACCTTGGG	AGCCAGTTAT	3960
TTTGCCATGG	CCTTGATTGC	AACAGCTGCC	TCCTCTGTCA	TGGCAGACAG	CACCGTGATC	4020
AGGATCTCTT	CTCCACAGTC	GTACTTCTGC	TCAATCTCT	TGCCAAGGTC	TCCCTCAGGG	4080
AGACGAAGGT	CCTCTCGTAC	CTCCCCGCTG	TCCTGGAGCA	GTGATAGGTA	CCCATCTCTG	4140
ATCTTTGGAT	CC					4152

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGATCCAAAG	ATTGCGCACG	AGTGGCCACA	TCATGAACCT	CCAGGCCAG	CCCAAGGCTC	60
AGAACAAGCG	GAAGCGTTGC	CTCTTTGGGG	GCCAGGAACC	AGCTCCAAG	GAGCAGCCCC	120
CTCCCCTGCA	GCCCCCCAG	CAGTCCATCA	GAGTGAAGGA	GGAGCAGTAC	CTCGGGCAGG	180
AGGGTCCAGG	AGGGGCAGTC	TCCACCTCTC	AGCCTGTGGA	ACTGCCCCCT	CCTAGCAGCC	240
TGGCCCTGCT	GAACCTGTG	GTGTATGGGC	CTGAGCGGAC	CTCAGCAGCC	ATGCTGTCCC	300
AGCAGGTGGC	CTCAGTAAAG	TGGCCCAACT	CTGTGATGGC	TCCAGGGCGG	GGCCCGGAGC	360
GTGGAGGAGG	TGGGGGTGTC	AGTGACAGCA	GCTGGCAGCA	GCAGCCAGGC	CAGCCTCCAC	420
CCCAATTCAAC	ATGGAACTGC	CACAGTCTGT	CCCTCTACAG	TGCAACCAAG	GGGAGCCCGC	480
ATCCTGGAGT	GGGAGTCCCG	ACTTACTATA	ACCACCTGA	GGCACTGAAG	CGGGAGAAAG	540
CGGGGGGGCC	ACAGCTGGAC	CGCTATGTGC	GACCAATGAT	GCCACAGAAG	GTGCAGCTGG	600
AGGTAGGGCG	GCCCCAGGCA	CCCTGAATT	CTTTCACGC	AGCCAAGAAA	CCCCCAAACC	660
AGTCACTGCC	CCTGCAACCC	TTCCAGCTGG	CATTGCGCCA	CCAGGTGAAC	CGGCAGGTCT	720
TCCGGCAGGG	CCCACCGCCC	CCAAACCCGG	TGGCTGCCTT	CCCTCCACAG	AAGCAGCAGC	780
AGCAGCAGCA	ACCACAGCAG	CAGCAGCAGC	AGCCCTACCC	CAGATGCCGC		840
TCTTTGAGAA	CTTCTATTCC	ATGCCACAGC	AACCTCGCA	GCAACCCAG	GACTTTGGCC	900
TGCAGCCAGC	TGGGCCACTG	GGACAGTCCC	ACCTGGCTCA	CCACAGCATG	GCACCCTACC	960
CCTTCCCCCC	CAACCCAGAT	ATGAACCCAG	AACTGCGCAA	GGCCCTTCTG	CAGGACTCAG	1020
CCCCGCAGCC	AGCGCTACCT	CAGGTCCAGA	TCCCCTTCCC	CCGCCGCTCC	CGCCGCTCT	1080
CTAAGGAGGG	TATCCTGCCT	CCCAGCGCCC	TGGATGGGGC	TGGCACCAG	CCTGGGCAGG	1140
AGGCCACTGG	CAACCTGTTG	CTACATCACT	GGCCCTGCA	GCAGCCGCCA	CCTGGCTCCC	1200
TGGGGCAGCC	CCATCCTGAA	GCTCTGGGAT	TCCCGCTGGA	GCTGAGGGAG	TGCGAGCTAC	1260
TGCTGTATGG	GGAGAGACTA	GCACCCAATG	GCCGGGAGCG	AGAGGCTCCT	GCCATGGGCA	1320
GCGAGGAGGG	CATGAGGGCA	GTGAGCACAG	GGGACTGTGG	GCAGGTGCTA	CGGGGCGGAG	1380
TGATCCAGAG	CACGCGACGG	AGGCGCCGGG	CATCCCAGGA	GGCCAATTTG	CTGACCCTGG	1440
CCCAGAAGGC	TGTGGAGCTG	GCCTCACTGC	AGAATGCAAA	GGATGGCAGT	GGTTCTGAAG	1500
AGAAGCGGAA	AAGTGTATTG	GCCTCAACTA	CCAAGTGTGG	GGTGGAGTTT	TCTGAGCCTT	1560
CCTTAGCCAC	CAAGCGAGCA	CGAGAAGACA	GTGGGATGGT	ACCCCTCATC	ATCCCAGTGT	1620
CTGTGCTGTG	GCGAACTGTG	GACCCAACTG	AGGCAGCCCA	GGCTGGAGGT	CTTGATGAGG	1680
ACGGGAAGGG	TCTTGAACAG	AACCTGCTG	AGCACAAGCC	ATCAGTCATC	GTACCCCGCA	1740
GGCGGTCCAC	CCGAATCCCC	GGGACAGATG	CTCAAGCTCA	GGCGGAGGAC	ATGAATGTCA	1800
AGTTGGAGGG	GGAGCCTTCC	GTGCGGAAAC	CAAAGCAGCG	GCCAGGCCCC	GAGCCCTCA	1860
TCATCCCCAC	CAAGGCGGGG	ACTTTCATCG	CCCCTCCCGT	CTACTCCAAC	ATCACCCCAT	1920
ACCAGAGCCA	CCTGCGCTCT	CCCGTGCGCC	TAGCTGACCA	CCCTCTGAG	CGGAGCTTTG	1980
AGCTACCTCC	CTACAGCCCG	CCCCCATCC	TCAGCCCTGT	GCGGGAAGGC	TCTGGCCTCT	2040

ACTTCAATGC	CATCATATCA	ACCAGCACCA	TCCCTGCCCC	TCCTCCCATC	ACGCCTAAGA	2100
GTGCCCATCG	CACGCTGCTC	CGGACTAACA	GTGCTGAAGT	AACCCCGCCT	GTCTCTCTG	2160
TGATGGGGGA	GGCCACCCCA	GTGAGCATCG	AGCCACGGAT	CAACGTGGGC	TCCCGGTTCC	2220
AGGCAGAAAT	CCCCTTGATG	AGGGACCGTG	CCCTGGCAGC	TGCAGATCCC	CACAAGGCTG	2280
ACTTGGTGTG	GCAGCCATGG	GAGGACCTAG	AGAGCAGCCG	GGAGAAGCAG	AGGCAAGTGG	2340
AAGACCTGCT	GACAGCCGCC	TGCTCCAGCA	TTTTCCCTGG	TGCTGGCACC	AACCAGGAGC	2400
TGGCCCTGCA	CTGTCTGCAC	GAATCCAGAG	GAGACATCCT	GGAAACGCTG	AATAAGCTGC	2460
TGCTGAAGAA	GCCCTTGCGG	CCCCACAACC	ATCCGCTGGC	AACCTATCAC	TACACAGGCT	2520
CTGACCAGTG	GAAGATGGCC	GAGAGGAAGC	TGTTCAACAA	AGGCATTGCC	ATCTACAAGA	2580
AGGATTTCTT	CCTGGTGAG	AAGCTGATCC	AGACCAAGAC	CGTGGCCAG	TGCGTGGAGT	2640
TCTACTACAC	CTACAAGAAG	CAGGTGAAAA	TCGGCCGCAA	TGGGACTCTA	ACCTTTGGGG	2700
ATGTGGATAC	GAGCGATGAG	AAGTCGGCCC	AGGAAGAGGT	TGAAGTGGAT	ATTAAAGACTT	2760
CCCAAAAGTT	CCCAAGGGTG	CCTCTTCCA	GAAGAGAGTC	CCCAAGTGAA	GAGAGGCTGG	2820
AGCCCAAGAG	GGAGGTGAAG	GAGCCAGGA	AGGAGGGGGA	GGAGGAGGTG	CCAGAGATCC	2880
AAGAGAAGGA	GGAGCAGGAA	GAGGGCGGAG	AGCGCAGCAG	CGGGGCAGCG	GCAGTCAAAG	2940
CCACGCAGAC	ACTACAGGCC	AATGAGTCGG	CCAGTGACAT	CCTCATCCTC	CGGAGCCACG	3000
AGTCCAACGC	CCCTGGGTCT	GCCGGTGGCC	AGGCCTCGGA	GAAGCCAAGG	GAAGGGACAG	3060
GGAAGTCACG	AAGGGCACTA	CCTTTTTCAG	AAAAAAAAAA	AAAAAACAA	AAAGCTT	3117

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAATTCGGCA	CGAGGTCAGT	TTCTGTGGA	ACACAGAGGC	TGCTGTCCC	ATTGAGACAA	60
CGACGGATAC	AGACCAAGCT	TGCTCTATAA	GGGATCCCAA	CAGTGGATT	GTGTTTAATC	120
TTAATCCGCT	AAACAGTTCG	CAAGGATATA	ACGTCTCTGG	CATTGGGAAG	ATTTTTATGT	180
TTAATGTCTG	CGGCACAATG	CCTGTCTGTG	GGACATCCT	GGGAAAACCT	GCTTCTGGCT	240
GTGAGGCAGA	AACCCAAACT	GAAGAGCTCA	AGAATTGGAA	GCCAGCAAGG	CCAGTCGGAA	300
TTGAGAAAAG	CCTCCAGCTG	TCCACAGAGG	GCTTCATCAC	TCTGACCTAC	AAAGGGCCTC	360
TCTCTGCCAA	AGGTACCGCT	GATGCTTTTA	TCGTCCGCTT	TGTTTGCAAT	GATGATGTTT	420
ACTCAGGGCC	CCTCAAATTC	CTGCATCAAG	ATATCGACTC	TGGGAAGGG	ATCCGAAACA	480
CTTACTTTGA	GTTTGAAACC	CGGTTGGCCT	GTGTTCTTTC	TCCAGTGGAC	TGCCAAGTCA	540
CCGACCTGGC	TGGAATGAG	TACGACCTGA	CTGGCCTAAG	CACAGTCAGG	AAACCTTGGA	600
CGGCTGTTGA	CACCTCTGTC	GATGGGAGAA	AGAGGACTTT	CTATTTGAGC	GTTTGCAATC	660
CTCTCCCTTA	CATTCTGGA	TGCCAGGGCA	GCGCAGTGGG	GTCTTGCTTA	GTGTCAGAAG	720
GCAATAGCTG	GAATCTGGGT	GTGGTGCAGA	TGAGTCCCA	AGCCGCGGCG	AATGGATCTT	780
TGAGCATCAT	GTATGTCAAC	GGTGACAAGT	GTGGGAACCA	GCGCTTCTCC	ACCAGGATCA	840
CGTTTGAGTG	TGCTCAGATA	TCGGGCTCAC	CAGCATTTCA	GCTTCAGGAT	GGTTGTGAGT	900
ACGTGTTTAT	CTGGAGAACT	GTGGAAAGCCT	GTCCCGTTGT	CAGAGTGGAA	GGGGACAACCT	960
GTGAGGTGAA	AGACCCAAGG	CATGGCAACT	TGTATGACCT	GAAGCCCTCG	GGCCTCAACG	1020
ACACCATCGT	GAGCGCTGGC	GAATACACTT	ATTACTTCCG	GGTCTGTGGG	AAGCTTTCTT	1080
CAGACGCTCG	CCCCACAAGT	GACAAGTCCA	AGGTGGTCTC	CTCATGTGAG	GAAAAGCGGG	1140
AACCCGAGGG	ATTTACAAA	GTGGCAGGTC	TCCTGACTCA	GAAGCTAACT	TATGAAAATG	1200
GCTTGTTAAA	AATGAACCTC	ACGGGGGGGG	ACACTTGCCA	TAAGGTTTAT	CAGCGCTCCA	1260
CAGCCATCTT	CTTCTACTGT	GACCGCGGCC	CCAGCGGGCC	AGTATTTCTA	AAGGAGACTT	1320
CAGATTGTTT	CTACTTGTTT	GAGTGGCGAA	CGCAGTATGC	CTGCCACCTT	TTGATCTGTA	1380
CTGAATGTTT	ATTCAAAGAT	GGGGCTGGCA	ACTCCTTCGA	CCTCTCGTCC	CTGTCAAGGT	1440
ACAGTGACAA	CTGGGAAGCC	ATCACTGGGA	CGGGGACCC	GGAGCACTAC	CTCATCAATG	1500
TCTGCAAGTG	TCTGGCCCCG	CAGGCTGGCA	CTGAGCCGTG	CCCTCCAGAA	GCAGCCCGGT	1560
GTCTGCTGGG	TGGCTCCAAG	CCCGTGAACC	TCGGCAGGGT	AAGGGACGGA	CCTCAGTGGA	1620
GAGATGGCAT	AATTGTCCTG	AAATACGTTG	ATGGCGACTT	ATGTCCAGAT	GGGATTCGGA	1680
AAAAGTCAAC	CACCATCCGA	TTCACTGCA	GCGAGAGCCA	AGTGAATCC	AGGCCATATG	1740
TCATCAGCGC	CGTGGAGGAC	TGTGAGTACA	CCTTTGCCTG	GCCACAGCC	ACAGCCTGTC	1800
CCATGAAGAG	CAACGAGCAT	GATGACTGCC	AGGTCAACAA	CCCAAGCACA	GGACACCTGT	1860
TTGATCTGAG	CTCCTTAAGT	GGCAGGGCGG	GATTACAGC	TGCTTACAGC	GAGAAGGGGT	1920
TGGTTTACAT	GAGCATCTGT	GGGGAGAATG	AAAAGTCCCC	TCCTGGCGTG	GGGGCCTGCT	1980
TTGGACAGAG	CAGGATTAGC	GTGGGCAAGG	CCAACAAGAG	GCTGAGATAC	GTGGACCAGG	2040
TTCCTGAGCT	GGTGTAACAG	GATGGGTCCC	CTTGTCCTTC	CAAAATCCGG	CTGAGCTATA	2100
AGAGTGTGAT	CAGTTTCGTG	TGCAGGCCCTG	AGGCCGGGCC	AACCAATAGG	CCCATGCTCA	2160
TCTCCCTGGA	CAAGCAGACA	TGCACTCTCT	TCTTCTCCTG	GCACACGCGG	CTGGCCTGCG	2220
AGCAAGCGAC	CGAATGTTCC	GTGAGGAATG	GAAGCTCTAT	TGTTGACTTG	TCTCCCTTA	2280
TTGATCGCAC	TGGTGGTTAT	GAGGCTTATG	ATGAGAGTGA	GGATGATGCC	TCCGATACCA	2340
ACCCTGATTT	CTACATCAAT	ATTTGTGAGC	CACTAAATCC	CATGCACGGA	GTGCCCTGTC	2400
CTGCCGGAGC	CGCTGTGTGC	AAAGTTCCTA	TTGATGGTCC	CCCCATAGAT	ATCGGCCGGG	2460
TAGCAGGACC	ACCAATACTC	AATCCAATAG	CAATGAGAT	TTACTTGAAT	TTTGAAGCA	2520

GTACTCCTTG	CCAGGAATTC	AGTTGTAAAT	AAAATTGAAC	CTGCTCAACA	GCTGAGGGAG	2580
ACTAGAAATG	ATGGGTCCAT	ATCCTGGTGC	ATTGTCATAC	AAITCAAACA	ATGGTGCAGC	2640
TACCAAGCTTG	TAATTTTATG	GGACTGCAAA	CAAGGCTTTT	TCTTGAAGCT	GAACCAAGAA	2700
CAACTTCTTA	TGTTCTTAG	GCTTTGTAAT	ATGTGCAGGA	ATATATGGAT	ACTGAGGAGG	2760
TTCAAAATTT	GGTCTCCACC	AGTTACCAAT	GCAATCGTCA	ATGACCCAGT	CTTGCAAAAC	2820
TCCATCCTGA	CGACCCAGTA	TCTCTGTCAT	TAAGCGTTTT	AGTCCITCAA	CTTCATCTTC	2880
TCTTGGGTGA	AGTTTACCA	CAGGTAGTTT	GAAGAAAGTT	GTTCACAGCT	GCAGCAGTAA	2940
CACATGGGGT	AGCCGGTGCT	CATGTACAAT	CAGAACCCTT	TCTACAGTCC	TCCTCATTC	3000
AATTTTATCA	AATTCCTTCC	TCATGCGCTG	AAATCTGGCT	GCAACAGAGC	TGTCCTTCTC	3060
GTAGAGGGGC	TCTTTTGTAC	CAAAAGTATA	ATTGGTAAGA	GGGTACAGGT	TGATGGTGCG	3120
CTCCAGGGTG	AGGGGCTTCG	TCTGCTGGAT	GTACTTGTG	CCGAAGTGA	TGACCCCGCG	3180
GGGCCAGCCG	GTCTGCGAGC	GATTGGGCGG	TACCACAGAC	ATGCTGGCGA	GCTCCGGCGC	3240
TGACGGCGAG	CAGAAAGTGG	CAGGCAGGGT	AGACTTTCCC	CGTGCGGGAA	GCCTCGTGCC	3300
GAATTC						3306

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4218 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAATTCGGCA	CGAGAATGGA	TCAACCTCAA	CAACACGTTA	AAGCTAGACG	AAAGAAGTAA	60
TACACAGTGT	ATGAGTCTCA	CATGAAATAC	CCGGATGTAA	ATCCAAAGAA	ACAGGAAGCA	120
GATTGGTGGT	TGCCAGGGAC	AAGGGCGGTG	GGAGGAGAAA	ATGGAGAGTA	ACGGGACTTT	180
ACTTTTGGAG	TGATGAGAA	GTTTTGGAGC	TAGATAGAAG	TGGTGGTTGT	ACACCATTTG	240
GGATGTACTA	CCACTTAATT	GTTCACTTAA	AAAGTTAATT	TATGTGAATT	GCATCTTAAT	300
TAAAAACAAG	GATAACATTC	CAACTCCTGG	ACATTATCCT	TCCTTTCCAT	TTGATGTCAG	360
GCCCGTGTGA	GAATTCCTAT	CCGGTTTGGT	CACGTCACTT	AAGATGTGGA	GAAATTAGGA	420
CGCACAGTTA	AGAGGAAGGA	TAACACTGAT	TAAGGTAGTG	CTTTTCTAGG	TTTCCCTTAA	480
ACAATTTAAC	AGATGGATAG	TGGCACCAC	TACGAGATGG	AAAAACCAGC	GGAAGGAAGA	540
TTTGGGGGAG	AAGTTAAGTT	TGCTTTGGGC	CTGTGTTTTG	CAACCTGAGT	GTAAAAGACA	600
TATGTTAAGT	CTTCAGTGGC	GAACACTAA	AACTAGAAAT	GGATCAGAAT	TTTATCTTTG	660
GATGTGACTT	CTCAAGGATG	GTCTTGTAC	TTCAAGTCC	GGTCAATGA	CAAGATGGGC	720
AATCTTTTCC	TGAAGGTCCA	AGCACTGAA	CGTGGCAGGG	TGACCCGATT	CCGATTTGCT	780
TAGAACAATC	CTAGTTTCATG	CCTATTGTCC	CTCATGTAAT	TAATATCACT	CTCAAAATGT	840
CTCATTTTGT	GCAATAAATT	CTGCAACGTG	ATGGCGCGAC	TCTCGCGGCC	CGAGCGGCCG	900
GACCTTGTCT	TCGAGGAAGA	GGACCTCCCC	TATGAGGAGG	AAATCATGCG	GAACCAATTC	960
TCTGTCAAAAT	GCTGGCTTCA	CTACATCGAG	TTCAAAACAGG	GCGCCCCGAA	GCCCAGGCTC	1020
AATCAGCTAT	ACGAGCGGGC	ACTCAAGCTG	CTGCCCTGCA	GCTACAAACT	CTGGTACCGA	1080
TACCTGAAGG	CGCGTCGGGC	ACAGGTGAAG	CATCGCTGTG	TGACCGACCC	TGCTATGAA	1140
GATGTCAACA	ACTGTCTATG	GAGGGCCTTT	GTGTTTCATG	ACAAGATGCC	TGCTGTGTGG	1200
CTAGATTACT	GCCAGTTCCT	CATGGACCAG	GGGCGCGTCA	CACACACCCG	CCGCACCTTC	1260
GACCGTGCCC	TCCGGGCACT	GCCCATCACG	CAGCACTCTC	GAATTTGGCC	CCTGTATCTG	1320
CGCTTCTGTC	GCTCACACCC	ACTGCCTGAG	ACAGCTGTGC	GAGGCTATCG	GCGCTTCCTC	1380
AAGCTGAGTC	CTGAGAGTGC	AGAGGAGTAC	ATTGAGTACC	TCAAGTCAAG	TGACCGGCTG	1440
GATGAGGCGC	CCCAGCGCCT	GGCCACCGTG	GTGAACGACG	AGCGTTTCGT	GTCTAAGGCC	1500
GGCAAGTCCA	ACTACCAGCT	GTGGCACGAG	CTGTGCGACC	TCATCTCCCA	GAATCCGGAC	1560
AAGGTACAGT	CCCTCAATGT	GGACGCCATC	ATCCGCGGGG	GCCTCACCCG	CTTCACCGAC	1620
CAGCTGGGCA	AGCTCTGGTG	TTCTCTCGCC	GACTACTACA	TCCGACGCGG	CCATTTTCGAG	1680
AAGGCTCGGG	ACGTGTACGA	GGAGGCCATC	CGGACAGTGA	TGACCGTGCG	GGACTTCACA	1740
CAGGTGTTTG	ACAGCTACGC	CCAGTTCGAG	GAGAGCATGA	TCGCTGCAAA	GATGGAGACC	1800
GCCTCGGAGC	TGGGGCGCGA	GGAGGAGGAT	GATGTGGACC	TGGAGTGGCG	CCTGGCCCGC	1860
TTGAGGAGC	TCATCAGCCG	GCGGCCCTTG	CTCTCAACA	GCGTCTTGCT	GCGCCAAAAC	1920
CCACACCAAG	TGCACGAGTG	GCACAAGCGT	GTGCGCCTGC	ACCAGGGCCG	CCCCCGGGAG	1980
ATCATCAACA	CCTACACAGA	GGCTGTGCAG	ACGGTGGACC	CCTTCAAGGC	CACAGGCAAG	2040
CCCCACACTC	TGTGGGTGGC	GTTTGCCAAG	TTTATGAGG	ACAACGGACA	GCTGGACGAT	2100
GCCCCGTGTC	TCCTGGAGAA	GGCCACCAAG	GTGAACCTCA	AGCAGGTGGA	TGACCTGGCA	2160
AGCGTGTGGT	GTCAAGTGGG	AGAGCTGGAG	CTCCGACACG	AGAATACGTA	TGAGGCGTTG	2220
CGGCTGCTGC	GAAAGGCCAC	GGCGTGCCT	CCCCGCCGGG	CCGAGTACTT	TGATGGTTCA	2280
GAGCCCGTGC	AGAACCGCGT	GTACAAGTCA	CTGAAGGTCT	GGTCCATGCT	GCGCGACCTG	2340
GAGGAGAGCC	TCGGCACCTT	CCAGTCCACC	AAGGCCGTGT	ACGACCGCAT	CCTGGACCTG	2400
CGTATCGCAA	CACCCAGAGT	CGTCATCAAC	TATGCCATGT	TCCTGGAGGA	GCACAAGTAC	2460
TTGAGGAGTA	GCTTCAAGGC	GTACGAGCGC	GGCATCTCGC	TGTTCAAGTG	GCCCAACGTG	2520
TCCGACATCT	GGAGCACCTA	CCTGACCAAA	TTTATTGCCC	GCTATGGGGG	CCGCAAGCTG	2580
GAGCGGGCAC	GGGACCTGTT	TGAACAGGCT	CTGGACGGCT	CCCCCCCCAA	ATATGCCAAG	2640
ACCTTGTACC	TGCTGTACGC	ACAGCTGGAG	GAGGAGTGGG	GCCTGGCCCG	GCATGCCATG	2700
GCCGTGTACG	AGCGTGCCAC	CAGGGCCGTG	GAGCCCGCCC	AGCAGTATGA	CATGTTCAAC	2760

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ATCTACATCA AGCGGGCGGC CGAGATCTAT GGGGTACCC ACACCCGCGG CATCTACCAG 2820
AAGGCCATTG AGGTGCTGTC GGACGAGCAC GCGCGTGAGA TGTGCCTGCG GTTTGCAGAC 2880
ATGGAGTGCA AGCTCGGGGA GATTGACCGC GCCCGGGCCA TCTACAGCTT CTGCTCCAG 2940
ATCTGTGACC CCCGGACGAC CGGCGCGTTC TGGCAGACGT GGAAGGACTT TGAGGTCCGG 3000
CATGGCAATG AGGACACCAT CAAGGAAATG CTGCGTATCC GCGCGAGCGT GCAGGCCACG 3060
TACAACACGC AGGTCAACTT CATGGCCTCG CAGATGCTCA AGGTCTCGGC CAGTGCCACG 3120
GGCACCCTGT CTGACCTGGC CCTGGGCAG AGTGGCATGG ACGACATGAA GCTGCTGGAA 3180
CAGCGGGCAG AGCAGCTGGC GGCTGAGGCG GAGCGTGACC AGCCCTTGCG CGCCAGAGC 3240
AAGATCTGTG TCGTGAGGAG TGACGCTCC CGGGAGGAGC TGGCAGAGCT GGCACAGCAG 3300
GTCAACCCCG AGGAGATCCA GCTGGGCAG GACGAGGACG AGGACGAGAT GGACCTGGAG 3360
CCCAACGAGG TTCGGCTGGA GCAGCAGAGC GTGCCAGCCG CAGTGTGTTG GAGCCTGAAG 3420
GAAGACTGAC CCGTCCCCTC GTGCCGAATT CGGCACGAGC AAGACCAGCC CCCAGATCAT 3480
TTGCCCTAAA GGTTTCCCT CGAAGTCACA AATGTTTCAA GGAATCTCAA ATTTTACAAA 3540
GTTTGAAGTG TGGGCATTGG TGGCCTGTGG CTGTGCTCTC TCTCTGTAGC TGTGTTCTCC 3600
CTACATCCCT GAAAGGAAAG TGAGCCTGCT CCTCCATCCG CAGACCTCCC TTTCCAGCGC 3660
CCAGGGCATG GGGTGCTGTG AGGGCAGCAT GCTAGGTGTG ACCGTGCTCC TGGCCTCCAG 3720
GCCCGTGTCC CTCTGTCTC TAGCCCACTA AGGCCCTGGC CCATTTGTGC TAAACAGGCA 3780
GTCCGACCTA GAAAGAGCAG ACAATCTCTC TGGGTCACCA GTCTGGCTAG GAGCTGGTCT 3840
CCTGACTGGG ATCCAGGCTT TCTCCCCTGC CCATGTGAAT TCCAGGGGCG AGAGCCTGAA 3900
ATGTTGAACA CAGCACTGGC CAAAGAGATG TCACCGTGGG AACCGAGGCT CTCTTCTCCT 3960
CCTGCTGCTT TCTGTTGGT CAGAGTAGCT GAGGCTGTGC TGAGAGGAGT TGGAGTGCTG 4020
GTTTTACCCC TGGTTGGTGT GCTTTGCTTT GAGGGCATT AGAAAGCCCA GCCCAGCCCT 4080
TGCTCCTGCC CTGCACACAG CGGAGCGACT TTTCTAGGTA TGCTCTTGAT TTCTGCAGAA 4140
GCAGCAGGTG GCATGGAGCC AAGAGGAAAG GTGACTGAAA CTGTCCACTC ATAGCCCGGC 4200
TGCCGTATTG AGAGGGCT

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(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1187 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

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GAGCTCGCGC GCCTGCAGGT CGACACTAGT GGATCCAAAG AATTCGGCAC GAGGGAAACT 60
CAACGGTGTA CGAGTGGAGG ACAGGGACAG AGCCCTCTGT GGTGGAACGA CCCACCTCG 120
AGGAGCTTCC TGAGCAGGTG GCAGAAGATG CGATTGACTG GGGCGACTTT GGGGTAGAGG 180
CAGTGTCTGA GGGGACTGAC TCTGGCATCT CTGCCGAGGC TGCTGGAATC GACTGGGGCA 240
TCTTCCCGGA ATCAGATTCA AAGGATCTGT GAGGTGATGG GATAGACTGG GGAGACGATG 300
CTGTTGCTTT GCAGATCACA GTGCTGGAAG CAGGAACCCA GGCTCCAGAA GGTGTTGCCA 360
GGGGCCAGCA TGCCCTGACA CTGCTTGAAT ACCTGAGAC CCGGAATCAG TTCCTTGATG 420
AGCTCATGGA GCTTGAGATC TTCTTAGCCC AGAGAGCAGT GGAGTTGAGT GAGGAGGCAG 480
ATGTCCTGTC TGTGAGCCAG TTCCAGCTGG CTCCAGCCAT CCTGCAGGGC CAGACCAAAG 540
AGAAGATGGT TACCATGGTG TCAGTGCTGG AGGATCTGAT TGGCAAGCTT ACCAGTCTTC 600
AGCTGCAACA CCTGTTATG ATCCTGGCCT CACCAAGGTA TGTGGACCGA GTGACTGAAT 660
TCCTCCAGCA AAAGCTGAAG CAGTCCCAGC TGCTGGCTTT GAAGAAAGAG CTGATGGTGC 720
AGAAGCAGCA GGAGGCACTT GAGGAGCAGG CGGCTCTGGA GCCTAAGCTG GACCTGCTAC 780
TGGAGAAGAC CAAGGAGCTG CAGAAGCTGA TTGAAGCTGA CATCTCCAAG AGGTACAGCG 840
GGCGCCCTGT GAACCTGATG GGAACCTCTC TGTGACACCC TCCGTGTTCT TGCCTGCCCA 900
TCTTCTCCGC TTTTGGGATG AAGATGATAG CCAGGGCTGT TGTTTTGGGG CCCTTCAAGG 960
CAAAAGACCA GGCTGACTGG AAGATGGAAG GCCACAGGAA GGAAGCGGCA CCTGATGGTG 1020
ATCTTGGCAC TCTCCATGTT CTCTACAAGA AGCTGTGGTG ATTGGCCCTG TGGTCTATCA 1080
GGCGAAAACC ACAGATTCTC CTCTAGTTA GTATAGCGCA AAAAGCTTCT CGAGAGTACT 1140
TCTAGAGCGG CCGCGGGCCC ATCGATTTTC CACCCGGGTG GGGTACC 1187

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(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

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CCCTCACTAA AGGGAACAAA AGCTGGAGCT CGCGCGCCTG CAGGTGCACA CTAGTGGATC 60
GAAAGTTCTG TACGCCAAGC TCGAAATTA CTCTGGGCTG ACCCATAAAC ATTTGTCTGA 120

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TCTAGGATAT AGTTGCGTTT CTTGCGGGCA GCAATCTGGA TGAGGCGGTT GAGGCACTGG 180
GTGGCGCTGCT GGATCAGGAC ATCCACGCGG CCAGCATAGT TCCGCTGCCG GCGTAGGCC 240
ATCACCCGCA TCTTATCCAT GATGGCATTG GTACCCAGGA GTTTGTAATT CTTGGAAGGG 300
TTGGAGGCTG CATGTTTGAT GGCCCATGTG GTCTTGCCAG CAGCAGGCAG GCCCACCATC 360
ATCAGAATCT CACATTCTGC CTTGCTCTTT GGTCCAACGG TGCCCGGAT ACGCTCACTA 420
AGGGGAAGGT GCTGGATGAA GGTAAACCCC GGGAGGACAG AACAGTAGGG CTCTGCTCTC 480
TGTCCGAAGT TGAATCCAC TCGCAATTTC TTACCCAGGA CATGAGGATA GAGGGCCTGA 540
CCCCCAAGG CTTCTTCTG GATTGCGAAA GCAATGCCCA TCCACTTTCC ATTCTTGGTA 600
AAAGACAGTT CCACGTCATT TCCACATTCA AAATCCGCAA AGCAGCCAAT CACCGGAGAG 660
CTCTGCGGTG CTAGGAGAGC GGCTGGGCCC GCAGACTGGG GGGAAAGCTC CGCAGCCGCA 720
GTGGGCCCCA GGATCAGGCC CCGCGTGGCC TGGAGAAGCC CAGTCTGGGC TGGAGCGGGA 780
GCTGGACAGT GTGGCCTTGC GTTCGCCCCC GGGAGCGCTG CAGTGTGCGC GGCCTCGGGT 840
GGATTTGCTG AGCACCAATA CCTCACGGTT GCCAACCTGG GGTTTTAGCT CCCTTGGTTT 900
TAATCCCTTA GGGGCGGGTG GGGGCACGGG AGGAAGGATG GGCCAGCTGG GTGCAATCCT 960
GCTGTAAAGC AGCCATTCTT TGATTTCTTA GAATTAAC TAACGGTCGCG CCGGAGGCCG 1020
CGGGGGCCGG AGCGGAGCAG CCGCGGTGTA GGTTCCCGAG TCGGCGCGTC GGGGCTGCCG 1080
TCCGCGCCCG GGACCCCGGC CTCTGGCCGC GCCGGCTCCG GCCTCCGGGG GGGCCGGGGC 1140
CGCCGGGACA TGGTGCCAGT CGCACCCCTT CCGCGCCGCC GCTGAGCTCG CCGGCGCGCG 1200
CCGGGCTGGG ACGTCCGAGC GGGGAAGATG TTTCCGCCCT GAAGAAGCTG GTGGGGTCGG 1260
ACCAAGCCCC GGGCCGGGAC AAGAATATCC CCGCCGGGCT GCAGTCCATG AACCAGGCGT 1320
TGCAAGAGCG CTTCGCCAAG GGGGTGCAGT ACAACATGAA GATAGTGATC CGGGGAGACA 1380
GGAACACGGG CAAGACACGG CTGTGGCACC GCCTGCAGGG CCGGCCGTTT GTGGAGGAGT 1440
ACATCCCCAC ACAGGAGATC CAGGTACCA GCATCCACTG GAGCTACAAG ACCACGGATG 1500
ACATCGTGAA GGTGAAGTC TGGATGTAG TAGACAAAGG AAAATGCAAA AAGCGAGGCG 1560
ACGGCTTAAA GATGGAGAAC GACCCCAAG AGNCGGAGT TGAAATGGCC CTGGATGCTG 1620
AGTTCTGGA CGTGACAAG AACTGCAACG GGGTGGTCAT GATGTTGAC ATTACCAAGC 1680
AGTGACCTT CAATTACAT CTCCGGGAGC TTCCAAAAGT GCCACCCAC GTGCCAGTGT 1740
GCGTGCTGGG GAATACCGG GACATGGCG AGCACCGAGT CATCTGCCG GACGACGTGC 1800
GTGACTTCAT CGACAACCTG GACAGACCTC CAGGTTCTCT CTACTTCCGC TATGCTGAGT 1860
CTTCCATGAA GAACAGCTTC GGCTAAAGT ACCTTCATA GTTCTTCAAT ATCCCATTTT 1920
TGCACTTCA GAGGGAGAGC CTGTTGCGG AGCTGGAGAC GAACCACTG GACATGGACG 1980
CCACGCTGGA GGAGCTGTG GTGCAGCAGG AGACGGAGGA CCAGAACTAC GGCATCTTCC 2040
TGGAGATGAT GGAGGCTCGC AGCCGTGGCC ATGCGTCCCC ACTGGCGGCC AACGGGCAGA 2100
GCCCATCCCC GGGCTCCAG TCACCACTCC TGCTTGACC CGCTGTGTC ACGGGAGCT 2160
CCAGCCCCGG CACACCCAG CCGCCCCAC AGCTGCCCT CAATGCTGCC CCACCATCCT 2220
CTGTGCCCCC TGTACACCC TCAGAGGCC TGCCCCACC TGCGTGCCCC TCAGCCCCCG 2280
CCCCACGGG CAGCATATC TTAGGCTGT TTGGGACGTC ACCTGCCACC GAGGCAGCCC 2340
CTCCACCTCC AGAGCCAGTC CCGGCCGCAC AGGGCCAGC AACGGTCCAG AGTGTGGAGG 2400
ACTTTGTTCC TGACGACCGC CTGGACGCA GCTTCTGGA AGACACAACC CCCGCCAGGG 2460
ACGAGAAGAA GGTGGGGGCC AAGGCTGCC AGCAGGACAG TGACAGTAT GGGGAGGGCC 2520
TGGGCGGCAA CCCGATGGT GCAGGGTTC AGGACGATG GGACCTCGAA GACCAGCCAC 2580
GTGGGAGTCC CCCGCTGCT GCAGGCCCG TCCCAGTCA AGACATCACT CTTTCGAGTG 2640
AGGAGGAAGC AGAAGTGGA GCTCCACAA AAGGCCCTGC CCCAGCTCCC CAGCAGTGT 2700
CAGAGCCAGA GACCAAGTGG TCCTCCATAC CAGCTTCGAA GCCACGGAGG GGGACAGCTC 2760
CCACGAGGAC CGCAGCACCC CCTGGCCAG GCGGTGTCT TGTTCGCACA GGTCCGGAGA 2820
AGCGCAGGAG CACCAAGGCC CCTGCTGAGA TGGAGCCGGG GAAGGGTGAG CAGGCCTCCT 2880
CGTCGGAGAG TGACCCGAG GGACCCATTG CTGCACAAAT GCTGTCTTC GTCATGGATG 2940
ACCCGACTT TGAGAGCGAG GGATCAGACA CACAGCGCAG GCGGATGAC TTTCCCGTGC 3000
GAGATGACCC CTCCGATGT ACTGACGAG ATGAGGGCCC TGCCGAGCCG CCCCACCCC 3060
CCAAGCTCCC TCTCCCCGCC TTCAGACTGA AGAATGACTC GGACCTCTTC GGGCTGGGGC 3120
TGGAGGAGGC CGACCCCAAG GAGAGCAGTG AGGAAGGTAA GGAGGGCAAA ACCCCCTCTA 3180
AGGAGAAGAA AAAAAAACA AAAAGCTTCT CGAGAGTACT TCTAGAGCGG CCGCGGGCCC 3240
ATCGATTTTC CACCCGGGTG GGTACCAGG TAAGTGATCC CAATTCGCC TATAGTGAGT 3300
CGTATT

```

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGCGGGGCCA GAGTGGGCTG

20

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCAGTCCTGG CCTGCGGATG

20

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GTCGACAGGA GAATTGGTTC

20

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCCTGGGTTC GGTGCGGGAC

20

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TGGTCGGGTG TTTGTGAGTG

20

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CCTCTCCGT CTCCTCAGTG

20

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GGATTGCTAG TCTCACAGAC

20

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TTAAGGGTGG CTGAAGGGAC

20

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ACCTTCCCTC CCTGTCACAG

20

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TGGTCGGGTG TTTGTGAGTG

20

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ACACCATTC AGAAATTCAG

20

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AAACTGCAGG TGGCTGAGTC

20

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GTCTAATGT TTTCAGGGAG

20

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AAACCTATG GTTACAATTC

20

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TCCTAGACAT GGTCAAGTG

20

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GATATAATTA GTTCTCCATC

20

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATGCCTGTTC CAGGCTGCAC

20

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GGACGGCGAC CTCCACCCAC

20

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GGGCTCCTCC GACGCCTGAG

20

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AGTCTAGCCC TGGCCTTGAC

20

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GTCCTGGGG ACTCCGGCAG

20

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CAGCTTTCCC TGGGCACATG

20

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CACAGCTGTC TCAAGCCAG

20

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

ACTGTTCCCC CTACATGATG

20

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

ATCATATCCT CTTGCTGGTC

20

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GTTCCCAGAG CTTGTCTGTG

20

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GTTTGGCAGA CTCATAGTTG

20

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TAGCAGGGAG CCATGACCTG

20

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CTTGGCGCCA GAAGCGAGAG

20

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CCTCTCTCTC TCTCTCTCTC

20

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

TCCCCGCTGA TTCCGCCAAG

20

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CTTTTGAAT TCGGCACGAG

20

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CCCCTGGTCC GCACCAAGTTC

20

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GAGAAGGGTC GGGGCGGCAG

20

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

AAATCACATC GCGTCAACAC

20

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TAAGAGAGTC ATAGTTACTC

20

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GCTCTAGAAG TACTCTGAG

20

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

ACTCTGGCCA TCAGGAGATC

20

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CAGGCGTTGT AGATGTTCTG

20

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

AGTGGCAGGC AGAAGTAATG

20

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GGTTGGAGAA CTGGATGTAG

20

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

CTATTGAGAT GCAACGCCAG

20

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CCATGGCACA CAGAGCAGAC

20

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GCTACCATGC AGAGACACAG

20

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CAGGCTGACA AGAAAATCAG

20

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGCACGCATA GAGGAGAGAC

20

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

TGGGTGATGC CTTTGCTGAC

20

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

AAAACAAGAT CAAGGTGATG

20

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

TTGCCACAT TGCTATGGTG

20

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GACCAAGATC AGAAGTAGAG

20

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CCCCTGGGCC AATGATGTTG

20

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

TCTTCCCACC ATAGCAATG

19

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

TGGTCTTGGT GACCAATGTG

20

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ACACCTCGGT GACCCCTGTG

20

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

TCTCCAAGTT CGGCACAGTG

20

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

ACATGGGCTG CACTCAGAC

20

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GATCCTCTGA ACCTGCAGAG

20

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GGAAATGAGG TGGGGCGATC

20

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CTTTGCCTTG GACAAGGATG

20

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GCACCTGCCA TTGGGGTAG

20

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

GGTGAAGCC ATTGACGGTG

20

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

TGCGTCTCTC GTCGCTGCTG

20

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GCGGAAACTC TGTGGTGCTG

20

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

AGGATTGCCT TCCTCTACTG

20

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

TGTCTGTTTC ACCAGGGCAG

20

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

CCAGTGCCTC TATGCATGTC

20

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

AGGAAGCCCA CGCACACCAC

20

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CCCTTTGTTT CCTGATCTTC

20

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

CGCTCGGGAT CCAGGTCATC

20

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

TCGAGGTTCAGAGCTAGTG

20

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

TCTTGGATCT CTGGCACCTC

20

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

CCATCAGAGT GAAGGAGGAG

20

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

CCATCTTCCA CTGGTCAGAG

20

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CTCCTTCTCT TGGATCTCTG

20

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

TTACTTCAGC ACTGTTAGTC

20

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

AGGGAGGTCG CTCAAAGCTC

20

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

TGGGTCCACA GTTCGCACAG

20

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

CAACTCTGTG ATGGCTCCAG

20

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

AGCAGGGTTC TGTTCAAGAC

20

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

CCATTGGGTG CTAGTCTCTC

20

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

CAGCCATGCT GTCCAGCAG

20

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

CTGGACCTGA GGTAGCGCTG

20

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

ATAACCAACC TGAGGCACTG

20

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CCTGCAGGTC GACACTAGTG

20

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

AATTGGAATG AGGAGGACTG

20

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GCTCTAGAAG TACTCTCGAG

20

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

ATTGTATGAC AATGCACCAG

20

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

TCCACAGAGG GCTTCATCAC

20

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

CCTGACTGGC CTAAGCACAG

20

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

AAGCCTCATA ACCACCAAGTG

20

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TGTCAACGGT GACAAGTGTG

20

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

TTGTACACCA GCTGCAGGTC

20

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GGGTGTGGTG CAGATGAGTC

20

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

ATCACACTCT TATAGCTCAG

20

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GTGGGAAGCT TTCCTCAGAC

20

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

TGATGAACAT GGCCTGGAG

20

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CATTGTGGAT GTACTACCAC

20

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

TGTGTTTTC AACCTGAGTG

20

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

ATAGTGGCAC CACTTACGAG

20

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

AATTCTGCAA CGTGATGGCG

20

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

CACAAGATGC CTCGTCTGTG

20

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

AATCCGGACA AGGTACAGTC

20

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

GCACGAGTGG CACAAGCGTG

20

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

GCAAGCGTGT GGTGTCAGTG

20

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

TGTTTGAACA GGCTCTGGAC

20

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

CGGCATGGCA ATGAGGACAC

20

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

AGGACGAGAT GGACCTCCAG

20

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

CCCTCTGTCC TCTAGCCAC

20

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

TCTTGAGGGG ACTGACTCTG

20

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

TGAGTGAGGA GGCAGATGTC

20

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

TGGCTTTGAA GAAAGAGCTG

20

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

GCAAAAGACC AGGCTGACTG

20

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

TGCAGCTCCT TGGTCTTCTC

20

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

GATTCACAGT CCCAAGGCTC

20

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

ATCTGGATGA GCGGTTGAG

20

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

GGTCACTCTC CGACGAGGAG

20

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

GGATCCAAAG TTCGTCTCTG

20

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

CGCTGTGTGT CTGATCCCTC

20

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

ATGAAGGTAA ACCCCGGGAG

20

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

TGGTCTCTGG CTCTGAGCAC

20

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

GCCTGGAGAA GCCCAGTCTG

20

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

CACACTCTGG ACCGTTGCTG

20

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

AAAGCTCCGC AGCCGAGTG

20

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

TCTTCCAGGA AGCTGCGGTC

20

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

GATGGTGGGG CAGCATTGAG

20

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

GTCACCAGTG GTGCCTGCAG

20

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

ACCTCACGGT TGCCAACCTG

20

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

CGCAACAGCG TCTCCCTCTG

20

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

AGTACCTTCA TAAGTTCTTC

20

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

TCCCAGACTT CAACCTTCAC

20

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

AAACATCTTC CCGGTCGGAC

20

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

GCTGAGCACC TTTACCTCAC

20

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

GACGTCCGTC CGGGAAGATG

20

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

ACACAGGAGA TGCAGGTAC

20

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

GAGTCTTCCA TGAAGAACAG

20

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

GCAGTGAGGA AGGTAAGGAG

20

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4047 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 378...1799
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

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GGATCCAAAG GACGCCCCCG CCGACAGGAG AATTGGTTCC CGGGCCCCGG GCGATGCCCC 60
CCCCGTAGCT CGGGCCCCGTG GTCGGGTGTT TGTGAGTGTT TCTATGTGGG AGAAGGAGGA 120
GGAGGAGGAA GAAGAAGCAA CGATTGTCT TCTCGGCTGG TCTCCCCCG GCTCTACATG 180
TTCCCCGCAC TGAGGAGACG GAAGAGGAGC CGTAGCCGCC CCCCTCCCG GCCCGGATTA 240
TAGTCTCTCG CCACAGCGGC CTCGGCCTCC CTTGGATTG AGACGCCGAT TCGCCAGTGT 300
TTTGGAAAT GGGAAAGTAAT GACAGCTGGC ACCTGAATA AGTACTTTTA TAGGCAACAC 360
CATTCCAGAA ATTCAGG ATG AAT GGG GAT ATG CCC CAT GTC CCC ATT ACT 410
          Met Asn Gly Asp Met Pro His Val Pro Ile Thr
              1             5             10

ACT CTT GCG GGG ATT GCT AGT CTC ACA GAC CTC CTG AAC CAG CTG CCT 458
Thr Leu Ala Gly Ile Ala Ser Leu Thr Asp Leu Leu Asn Gln Leu Pro
              15             20             25

CTT CCA TCT CCT TTA CCT GCT ACA ACT ACA AAG AGC CTT CTC TTT AAT 506
Leu Pro Ser Pro Leu Pro Ala Thr Thr Thr Lys Ser Leu Leu Phe Asn
              30             35             40

GCA CGA ATA GCA GAA GAG GTG AAC TGC CTT TTG GCT TGT AGG GAT GAC 554
Ala Arg Ile Ala Glu Glu Val Asn Cys Leu Leu Ala Cys Arg Asp Asp
              45             50             55

AAT TTG GTT TCA CAG CTT GTC CAT AGC CTC AAC CAG GTA TCA ACA GAT 602
Asn Leu Val Ser Gln Leu Val His Ser Leu Asn Gln Val Ser Thr Asp
              60             65             70             75

CAC ATA GAG TTG AAA GAT AAC CTT GGC AGT GAT GAC CCA GAA GGT GAC 650
His Ile Glu Leu Lys Asp Asn Leu Gly Ser Asp Asp Pro Glu Gly Asp
              80             85             90

ATA CCA GTC TTG TTG CAG GCC GTC CTG GCA AGG AGT CCT AAT GTT TTC 698
Ile Pro Val Leu Leu Gln Ala Val Leu Ala Arg Ser Pro Asn Val Phe
              95             100             105

AGG GAG AAA AGC ATG CAG AAC AGA TAT GTA CAA AGT GGA ATG ATG ATG 746
Arg Glu Lys Ser Met Gln Asn Arg Tyr Val Gln Ser Gly Met Met Met
              110             115             120

TCT CAG TAT AAA CTT TCT CAG AAT TCC ATG CAC AGT AGT CCT GCA TCT 794
Ser Gln Tyr Lys Leu Ser Gln Asn Ser Met His Ser Ser Pro Ala Ser
              125             130             135

TCC AAT TAT CAA CAA ACC ACT ATC TCA CAT AGC CCC TCC AGC CGG TTT 842
Ser Asn Tyr Gln Gln Thr Thr Ile Ser His Ser Pro Ser Ser Arg Phe
              140             145             150             155

GTG CCA CCA CAG ACA AGC TCT GGG AAC AGA TTT ATG CCA CAG CAA AAT 890
Val Pro Pro Gln Thr Ser Ser Gly Asn Arg Phe Met Pro Gln Gln Asn
              160             165             170

AGC CCA GTG CCT AGT CCA TAC GCC CCA CAA AGC CCT GCA GGA TAC ATG 938
Ser Pro Val Pro Ser Pro Tyr Ala Pro Gln Ser Pro Ala Gly Tyr Met
              175             180             185

CCA TAT TCC CAT CCT TCA AGT TAC ACA ACA CAT CCA CAG ATG CAA CAA 986
Pro Tyr Ser His Pro Ser Ser Tyr Thr His Pro Gln Met Gln Gln
              190             195             200

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GCA TCG GTA TCA AGT CCC ATT GTT GCA GGT GGT TTG AGA AAC ATA CAT 1034
 Ala Ser Val Ser Ser Pro Ile Val Ala Gly Gly Leu Arg Asn Ile His
 205 210 215

GAT AAT AAA GTT TCT GGT CCG TTG TCT GGC AAT TCA GCT AAT CAT CAT 1082
 Asp Asn Lys Val Ser Gly Pro Leu Ser Gly Asn Ser Ala Asn His His
 220 225 230 235

GCT GAT AAT CCT AGA CAT GGT TCA AGT GAG GAC TAC CTA CAC ATG GTG 1130
 Ala Asp Asn Pro Arg His Gly Ser Ser Glu Asp Tyr Leu His Met Val
 240 245 250

CAC AGG CTA AGT AGT GAC GAT GGA GAT TCT TCA ACA ATG AGG AAT GCT 1178
 His Arg Leu Ser Ser Asp Asp Gly Asp Ser Ser Thr Met Arg Asn Ala
 255 260 265

GCA TCT TTT CCC TTG AGA TCT CCA CAG CCA GTA TGC TCC CCT GCT GGA 1226
 Ala Ser Phe Pro Leu Arg Ser Pro Gln Pro Val Cys Ser Pro Ala Gly
 270 275 280

AGT GAA GGA ACT CCT AAA GGC TCA AGA CCA CCT TTA ATC CTA CAA TCT 1274
 Ser Glu Gly Thr Pro Lys Gly Ser Arg Pro Pro Leu Ile Leu Gln Ser
 285 290 295

CAG TCT CTA CCT TGT TCA TCA CCT CGA GAT GTT CCA CCA GAT ATC TTG 1322
 Gln Ser Leu Pro Cys Ser Ser Pro Arg Asp Val Pro Pro Asp Ile Leu
 300 305 310 315

CTA GAT TCT CCA GAA AGA AAA CAA AAG AAG CAG AAG AAA ATG AAA TTA 1370
 Leu Asp Ser Pro Glu Arg Lys Gln Lys Lys Gln Lys Lys Met Lys Leu
 320 325 330

GGC AAG GAT GAA AAA GAG CAG AGT GAG AAA GCG GCA ATG TAT GAT ATA 1418
 Gly Lys Asp Glu Lys Glu Gln Ser Glu Lys Ala Ala Met Tyr Asp Ile
 335 340 345

ATT AGT TCT CCA TCC AAG GAC TCT ACT AAA CTT ACA TTA AGA CTT TCT 1466
 Ile Ser Ser Pro Ser Lys Asp Ser Thr Lys Leu Thr Leu Arg Leu Ser
 350 355 360

CGT GTA AGG TCT TCA GAC ATG GAC CAG CAA GAG GAT ATG ATT TCT GGT 1514
 Arg Val Arg Ser Ser Asp Met Asp Gln Gln Glu Asp Met Ile Ser Gly
 365 370 375

GTG GAA AAT AGC AAT GTT TCA GAA AAT GAT ATT CCT TTT AAT GTG CAG 1562
 Val Glu Asn Ser Asn Val Ser Glu Asn Asp Ile Pro Phe Asn Val Gln
 380 385 390 395

TAC CCA GGA CAG ACT TCA AAA ACA CCC ATT ACT CCA CAA GAT ATA AAC 1610
 Tyr Pro Gly Gln Thr Ser Lys Thr Pro Ile Thr Pro Gln Asp Ile Asn
 400 405 410

CGC CCA CTA AAT GCT GCT CAA TGT TTG TCG CAG CAA GAA CAA ACA GCA 1658
 Arg Pro Leu Asn Ala Ala Gln Cys Leu Ser Gln Gln Glu Gln Thr Ala
 415 420 425

TTC CTT CCA GCA AAT CAA GTG CCT GTT TTA CAA CAG AAC ACT TCA GTT 1706
 Phe Leu Pro Ala Asn Gln Val Pro Val Leu Gln Gln Asn Thr Ser Val
 430 435 440

GCT GCA AAA CAA CCC CAG ACC AAT AGT CAC AAA ACC TTG GTG CAG CCT 1754
 Ala Ala Lys Gln Pro Gln Thr Asn Ser His Lys Thr Leu Val Gln Pro
 445 450 455

GGA ACA GGC ATA GAG GTC TCA GCA GAG CTG CCC AAG GAC AAG ACC TAAGA 1804
 Gly Thr Gly Ile Glu Val Ser Ala Glu Leu Pro Lys Asp Lys Thr
 460 465 470

TCCAGCAGGG AACTATGTAG TCACCCCGAG AGGCCAGCT CTCTCCGTGA GCTCTGGGCC 1864
 TAGGGTGGGG GTGGTTGTG GTTCTGCGCG CACTGTTCCC CCTACATGAT GGGTCCATCC 1924
 CAGTTGGCTT CTCTCACTCG CTTCTCTCTG TGGAGAAGCC TGTCAGGTG TCACTGCCTC 1984
 CAGGAAGCTG TCTCTGATT CTCCAGTTGA ACAGTGAGAT TTGCCACACC TCACATGCAT 2044
 CGCTCTTGTC CCTGGAATTG TAACCATAGG TTTTCCTGTC TCCTGGAGGA CAAGGATGAG 2104

GGCTTTCCAC TTGAGTCTCC CTGGTGGAGC CCAGCTCCTG ACATACCTGG TAAAAGTTCT 2164
 CAAGAGAAGA ACATGGAGGA GGAATGTGGA TAACAACCCCT GGCTGCCTGT GTGTTCACAG 2224
 CTAGGAAGAT GTAATGTCCC CACAAACGGG GTAAATGGCT TGCTGCGCT ACAGCTGTCT 2284
 CAAGCCAGG CCTGGGCGC CAGCCCAAGC CCAAGGACTA GGTCCAGAGC CACACAGCGC 2344
 CAGGCCACAT CCGCCTCACC TGGGACCCTT TGTGGGTAC AGTCTCCGGC CCCACCCAGA 2404
 CCTCCTGAAG GAGAGACCC ATGCAAGGA CTCACCCACC TGCAGTTTCA TAAGCCCCCA 2464
 GTGGGTTCCT AGGCATGAAG ACCACCGGTT AGAGGCTGAA CTGGCAGGAA CCTGTCTCCA 2524
 GCCCCTTCTC ACCCCAGCCG GGCCCTGCCT CAGAGGCAGC ACCCAGGACG TGGCCATGAC 2584
 CCGTGGACTC CACTCAATCC CTCTTCTCCA GGAGCCATGC AAAGTGTGAG CCAGCCAGGC 2644
 CCTTGGGAAG CAGTCATCAC CTCTTAAGGC ATTGTGGGTG TCGGTCTGCG AACTGCCAGG 2704
 TGCAGCACAC GACCCGTGTC CGGTGTTTCA TAGCAGGGAG CCATGACCTG GCAACGATTC 2764
 CACGCTCAAA GGGGCACCCG GGGGGCCCTG GGTGCGGGCG GATCAGCTTT CCTTGGGCAC 2824
 ATCTGCCTCA TTCCAGATCT CCAGGGCTCA TGTCTGTGAC AGGGAGGGAA GGCTCTGCC 2884
 TGGCCTTCCG TCAGCTCTGC CAGTGCAGGC TGGGCAGCCT GGGCTTTAGA GCTGGCTTCT 2944
 GCCCACACTT TCTCCGTGAA AGGAAAACAA CTATGAGTCT GCCAACGCA TCTCAGATGC 3004
 GTTTTAAAAA ATTCTGGTCC CCGCTCTCTG TCCCATCATC CGCCTCGGGG ACTTCTCTCT 3064
 TCCGTGGTTC TCACCCATA CTCTGTCACT GCCACATTT CACCTGGGCC TGGCCTTTGT 3124
 CTCCACCTGA AACTCCTGAA AATCTTGAAA TGGATTCTA GGTCACTGGG GACTCCGGCA 3184
 GCACATTCCG CTTCAGAATA AAGGGCGCCC GCGGTCCCCC AGCACCTCCC CAAGCCACAC 3244
 CCCTAGCTTC CCTCCTATC CTTGACGCCT GAGGGTCCCT TCAGCCACCC TTAAGTCCCC 3304
 ACCTGGGCTC CTGCCCCGCC CTTGGCTAGC AGCGCCTTCT CCACCGGGGC CCCCTCTGCT 3364
 CACAGAGCCC CCTCACCTCC CTGGGGATGA GGGGCCAGGC CATGACCCTG AAAGTCTAGC 3424
 CCTGGCCTTG ACCTCCAGG AGCGCCCTCC CCGCCCTCTC CCGGCCCGG CCCGTCCTC 3484
 TGCTGCTGGC CTCTGGGTG TCCCCGCGAG ACTGAGCTGC GCTTGGGGT CCTGGCGGCC 3544
 TGGGCCGTCC CGCACCGAAC CCAGGCGGTC GGAGCCCGGC GGAAGGCGC GAGGTCTTTC 3604
 TGGGGGCTCC TCCGACGCT GAGGGCGCTG CTTCCCGCG GCGGCCCGG GTTCTTGCGG 3664
 AGCCGGGGCC TCCGCTCTCG GGTGACCCGG TGAGACCCCG GGGGAGGCCG CTGGGAGGCC 3724
 GCGGGCTCTG CTCCCGGGTC CCAAACGAC TGCTGCCCC TCAGGAGGGA CGGCGACCTC 3784
 CACCCACGGC GCTGGCGCCC GCACGGCGCG TCCTCCCGCT CCCGACGCT GGACGCTTCC 3844
 CGAGGCGGCC CCGCCGGGCC CCACGCGCGG CCCCATCCG AGGCCAGGAC TGCTTCCCG 3904
 GAGCTGGCGG CCCCCAGCCT GGAGGAGCCG GCCCCAGACG CCCTCCAGC CCTCCCGAGC 3964
 CCACTCTGGC CCGCAGCCC CCGCTGGTC CGAGTGGGG TCTCTGGCCC GGGCCTTTC 4024
 CGGGGAAGGA AAGCAAAAAG CTT 4047

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Met Asn Gly Asp Met Pro His Val Pro Ile Thr Thr Leu Ala Gly Ile
 1 5 10 15
 Ala Ser Leu Thr Asp Leu Leu Asn Gln Leu Pro Leu Pro Ser Pro Leu
 20 25 30
 Pro Ala Thr Thr Thr Lys Ser Leu Leu Phe Asn Ala Arg Ile Ala Glu
 35 40 45
 Glu Val Asn Cys Leu Leu Ala Cys Arg Asp Asp Asn Leu Val Ser Gln
 50 55 60
 Leu Val His Ser Leu Asn Gln Val Ser Thr Asp His Ile Glu Leu Lys
 65 70 75 80
 Asp Asn Leu Gly Ser Asp Asp Pro Glu Gly Asp Ile Pro Val Leu Leu
 85 90 95
 Gln Ala Val Leu Ala Arg Ser Pro Asn Val Phe Arg Glu Lys Ser Met
 100 105 110
 Gln Asn Arg Tyr Val Gln Ser Gly Met Met Met Ser Gln Tyr Lys Leu
 115 120 125
 Ser Gln Asn Ser Met His Ser Ser Pro Ala Ser Ser Asn Tyr Gln Gln
 130 135 140
 Thr Thr Ile Ser His Ser Pro Ser Ser Arg Phe Val Pro Pro Gln Thr
 145 150 155 160
 Ser Ser Gly Asn Arg Phe Met Pro Gln Gln Asn Ser Pro Val Pro Ser
 165 170 175
 Pro Tyr Ala Pro Gln Ser Pro Ala Gly Tyr Met Pro Tyr Ser His Pro
 180 185 190
 Ser Ser Tyr Thr Thr His Pro Gln Met Gln Gln Ala Ser Val Ser Ser
 195 200 205

Pro Ile Val Ala Gly Gly Leu Arg Asn Ile His Asp Asn Lys Val Ser
 210 215 220
 Gly Pro Leu Ser Gly Asn Ser Ala Asn His His Ala Asp Asn Pro Arg
 225 230 235 240
 His Gly Ser Ser Glu Asp Tyr Leu His Met Val His Arg Leu Ser Ser
 245 250 255
 Asp Asp Gly Asp Ser Ser Thr Met Arg Asn Ala Ala Ser Phe Pro Leu
 260 265 270
 Arg Ser Pro Gln Pro Val Cys Ser Pro Ala Gly Ser Glu Gly Thr Pro
 275 280 285
 Lys Gly Ser Arg Pro Pro Leu Ile Leu Gln Ser Gln Ser Leu Pro Cys
 290 295 300
 Ser Ser Pro Arg Asp Val Pro Pro Asp Ile Leu Asp Ser Pro Glu
 305 310 315 320
 Arg Lys Gln Lys Lys Gln Lys Lys Met Lys Leu Gly Lys Asp Glu Lys
 325 330 335
 Glu Gln Ser Glu Lys Ala Ala Met Tyr Asp Ile Ile Ser Ser Pro Ser
 340 345 350
 Lys Asp Ser Thr Lys Leu Thr Leu Arg Leu Ser Arg Val Arg Ser Ser
 355 360 365
 Asp Met Asp Gln Gln Glu Asp Met Ile Ser Gly Val Glu Asn Ser Asn
 370 375 380
 Val Ser Glu Asn Asp Ile Pro Phe Asn Val Gln Tyr Pro Gly Gln Thr
 385 390 395 400
 Ser Lys Thr Pro Ile Thr Pro Gln Asp Ile Asn Arg Pro Leu Asn Ala
 405 410 415
 Ala Gln Cys Leu Ser Gln Gln Glu Gln Thr Ala Phe Leu Pro Ala Asn
 420 425 430
 Gln Val Pro Val Leu Gln Gln Asn Thr Ser Val Ala Ala Lys Gln Pro
 435 440 445
 Gln Thr Asn Ser His Lys Thr Leu Val Gln Pro Gly Thr Gly Ile Glu
 450 455 460
 Val Ser Ala Glu Leu Pro Lys Asp Lys Thr
 465 470

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2998 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 26...799
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

AAGCTTTTGTG AATTCGGCAC GAGAT GCT ACA CAG GCT ATA TTT GAA ATA CTG	52
Ala Thr Gln Ala Ile Phe Glu Ile Leu	
1 5	
GAG AAA TCC TGG TTG CCC CAG AAT TGT ACA CTG GTT GAT ATG AAG ATT	100
Glu Lys Ser Trp Leu Pro Gln Asn Cys Thr Leu Val Asp Met Lys Ile	
10 15 20 25	
GAA TTT GGT GTT GAT GTA ACC ACC AAA GAA ATT GTT CTT GCT GAT GTT	148
Glu Phe Gly Val Asp Val Thr Thr Lys Glu Ile Val Leu Ala Asp Val	
30 35 40	
ATT GAC AAT GAT TCC TGG AGA CTC TGG CCA TCA GGA GAT CGA AGC CAA	196
Ile Asp Asn Asp Ser Trp Arg Leu Trp Pro Ser Gly Asp Arg Ser Gln	
45 50 55	
CAG AAA GAC AAA CAG TCT TAT CGG GAC CTC AAA GAA GTA ACT CCT GAA	244
Gln Lys Asp Lys Gln Ser Tyr Arg Asp Leu Lys Glu Val Thr Pro Glu	
60 65 70	
GGG CTC CAA ATG GTA AAG AAA AAC TTT GAG TGG GTT GCA GAG AGA GTA	292

Gly 75	Leu	Gln	Met	Val	Lys	Lys	Asn	Phe	Glu	Trp	Val 85	Ala	Glu	Arg	Val	
GAG	TTG	CTT	TTG	AAA	TCA	GAA	AGT	CAG	TGC	AGG	GTT	GTA	GTG	TTG	ATG	340
Glu 90	Leu	Leu	Leu	Lys 95	Ser	Glu	Ser	Gln	Cys	Arg 100	Val	Val	Val	Leu	Met 105	
GGC	TCT	ACT	TCT	GAT	CTT	GGT	CAC	TGT	GAA	AAA	ATC	AAG	AAG	GCC	TGT	388
Gly	Ser	Thr	Ser	Asp 110	Leu	Gly	His	Cys	Glu	Lys 115	Ile	Lys	Lys	Ala	Cys 120	
GGA	AAT	TTT	GGC	ATT	CCA	TGT	GAA	CTT	CGA	GTA	ACA	TCT	GCG	CAT	AAA	436
Gly	Asn	Phe	Gly 125	Ile	Pro	Cys	Glu	Leu	Arg	Val 130	Thr	Ser	Gta	His	Lys 135	
GGA	CCA	GAT	GAA	ACT	CTG	AGG	ATT	AAA	GCT	GAG	TAT	GAA	GGG	GAT	GGC	484
Gly	Pro	Asp	Glu 140	Thr	Leu	Arg	Ile 145	Lys	Ala	Glu	Tyr	Glu	Gly	Asp	Gly 150	
ATT	CCT	ACT	GTA	TTT	GTG	GCA	GTG	GCA	GGC	AGA	AGT	AAT	GGT	TTG	GGA	532
Ile	Pro	Thr	Val	Phe	Val	Ala 160	Val	Ala	Gly	Arg 165	Ser	Asn	Gly	Leu	Gly	
CCA	GTG	ATG	TCT	GGG	AAC	ACT	GCA	TAT	CCA	GTT	ATC	AGC	TGT	CCT	CCC	580
Pro	Val	Met	Ser	Gly	Asn 175	Thr	Ala	Tyr	Pro	Val 180	Ile	Ser	Cys	Pro	Pro 185	
CTC	ACA	CCA	GAC	TGG	GGA	GTT	CAG	GAT	GTG	TGG	TCT	TCT	CTT	CGA	CTA	628
Leu	Thr	Pro	Asp 190	Trp	Gly	Val	Gln	Asp 195	Val	Trp	Ser	Ser	Leu	Arg 200	Leu	
CCC	AGT	GGT	CTT	GGC	TGT	TCA	ACC	GTA	CTT	TCT	CCA	GAA	GGA	TCA	GCT	676
Pro	Ser	Gly	Leu 205	Tyr	Cys	Ser	Thr 210	Val	Leu	Ser	Pro	Glu	Gly 215	Ser	Ala	
CAA	TTT	GCT	GCT	CAG	ATA	TTT	GGG	TTA	AGC	AAC	CAT	TTG	GTA	TGG	AGC	724
Gln	Phe	Ala	Ala 220	Gln	Ile	Phe 225	Gly	Leu	Ser	Asn 230	His	Leu	Val	Trp	Ser	
AAA	CTG	CGA	GCA	AGC	ATT	TTG	AAC	ACA	TGG	ATT	TCC	TTG	AAG	CAG	GCT	772
Lys	Leu	Arg	Ala 235	Ser	Ile 240	Leu	Asn 245	Thr	Trp	Ile 245	Ser	Leu	Lys	Gln	Ala	
GAC	AAG	AAA	ATC	AGA	GAA	TGT	AAT	TTA	TAAGAAAGAA	TGCCATTGAA	TTTTTTA					826
Asp 250	Lys	Lys	Ile	Arg 255	Glu	Cys	Asn	Leu								
GGGGAAAAAC	TACAAATTTC	TAATTTAGCT	GAAGGAAAAT	CAAGCAAGAT	GAAAAGGTAA											886
TTTTAAATTA	GAGAACACAA	ATAAAATGTA	TTAGTGAATA	AATGGTGAGG	GTAGGCCTAT											946
TCAGATGCCAA	GGCCAGCAAT	GGGGCTCCCC	ATTATCCCCA	CCCCCTTGGT	CCCAGTCCCC											1006
TTCTCTGCAA	TGGGCACGCA	TAGAGGAGAG	ACAAAGGGTA	TTAGACGCAA	CATCATTGGC											1066
CCAGGGGAGT	CCGAGAAGAG	CTGCCATTGG	CTGACAGGGC	ATTTCAGGC	TCTGTCAATTG											1126
GTACAGGGAGC	ACACCCCAAGC	CTGAAGAGTG	ATGCCATTGG	CCAGGGAGTG	GTTTTGTCAT											1186
AGCCGTTGGC	TGTGAAGTGG	AAGGAAAAGA	TCTGGGAATG	AAGCCCTGTG	GCCAGGAAGA											1246
TAGACAGGGC	AGCAACTTCT	GGGCCTCCAG	GCCCTCTCTC	CACCATAGCA	ATGTGGGCCAA											1306
AACTGGTGTG	AGGCCCAAGC	CTGAAGAAAG	AGCCCAAGCC	AGAGGGCAAG	TGACAAAGGA											1366
TGTACCATGT	CCAATCTCCC	ACACCCCTGGG	GCTGCCCTTC	CCAATGTCTT	CTGTGATAGC											1426
CAAGTTGGGC	TGGGAGCAGC	TCACTGTCTCC	TCTAGCCAGG	AGGGTTTCTC	AGCTCCTGGA											1486
GGCCGCAGCT	TGATGTTGAA	CTGCTGCAGG	GTCTGTCTCA	GCTGTTTCTG	GTTCCACGCA											1546
AAGTAGGGCG	ACACAGCATT	GTGGAAGAGC	AGCAGCTGTG	TGTGCATCAC	CTTGATCTTG					</						

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GCTGCCCTTT GGGAAAGGTCA CCAACCTCCT GATGCTGAAG GGGAAAAACC AGGCCTTCAT 2446
CGAGATGAAC ACGGAGGAGG CTGCCAATAC CATGGTGAAC TACTACACCT CGGTGACCCC 2506
TGTGCTGCGC GGCCAGCCCA TCTACATCCA GTTCTCCAAC CACAAGGAGC TGAAGACCGA 2566
CAGTCTCCCC AACCAGGCGC GGGCCAGGCG GGCCCTGCAG GCGGTGAACT CGGTCCAGTC 2626
GGGGAACCTG GCCTTGGCTG CCTCGGCGGC GGCCGTGGAT GCAGGGATGG CGATGGCCGG 2686
GCAGAGCCCC GTGCTCAGGA TCATCGTGGA GAACCTCTTC TACCCTGTGA CCCTGGATGT 2746
GCTGCACCAG ATTTTCTCCA AGTTCGGCAC AGTGTGAAG ATCATCACCT TCACCAAGAA 2806
CAACCAAGTT CAGGCCCTGC TGCAGTATGC GGACCCCGTG AGCGCCAGC ACGCCAAGCT 2866
GTGCTGGAGC GGGCAGAACA TCTACAACGC CTGCTGCACG CTGCGCATCG ACTTTTCCAA 2926
GCTCACCAGC CTCACGTCA AGTACAACAA TGACAAGAGC CGTGACTACC TCGTGCCGAA 2986
TTCTTTGGAT CC

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(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

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Ala Thr Gln Ala Ile Phe Glu Ile Leu Glu Lys Ser Trp Leu Pro Gln
 1          5          10          15
Asn Cys Thr Leu Val Asp Met Lys Ile Glu Phe Gly Val Asp Val Thr
          20          25          30
Thr Lys Glu Ile Val Leu Ala Asp Val Ile Asp Asn Asp Ser Trp Arg
          35          40          45
Leu Trp Pro Ser Gly Asp Arg Ser Gln Gln Lys Asp Lys Gln Ser Tyr
          50          55          60
Arg Asp Leu Lys Glu Val Thr Pro Glu Gly Leu Gln Met Val Lys Lys
65          70          75          80
Asn Phe Glu Trp Val Ala Glu Arg Val Glu Leu Leu Lys Ser Glu
          85          90          95
Ser Gln Cys Arg Val Val Val Leu Met Gly Ser Thr Ser Asp Leu Gly
          100          105          110
His Cys Glu Lys Ile Lys Lys Ala Cys Gly Asn Phe Gly Ile Pro Cys
          115          120          125
Glu Leu Arg Val Thr Ser Ala His Lys Gly Pro Asp Glu Thr Leu Arg
          130          135          140
Ile Lys Ala Glu Tyr Glu Gly Asp Gly Ile Pro Thr Val Phe Val Ala
          145          150          155          160
Val Ala Gly Arg Ser Asn Gly Leu Gly Pro Val Met Ser Gly Asn Thr
          165          170          175
Ala Tyr Pro Val Ile Ser Cys Pro Pro Leu Thr Pro Asp Trp Gly Val
          180          185          190
Gln Asp Val Trp Ser Ser Leu Arg Leu Pro Ser Gly Leu Gly Cys Ser
          195          200          205
Thr Val Leu Ser Pro Glu Gly Ser Ala Gln Phe Ala Ala Gln Ile Phe
          210          215          220
Gly Leu Ser Asn His Leu Val Trp Ser Lys Leu Arg Ala Ser Ile Leu
          225          230          235          240
Asn Thr Trp Ile Ser Leu Lys Gln Ala Asp Lys Lys Ile Arg Glu Cys
          245          250          255
Asn Leu

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(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1038 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

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Ile Gln Arg Phe Gly Thr Ser Gly His Ile Met Asn Leu Gln Ala Gln
 1          5          10          15

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Pro Lys Ala Gln Asn Lys Arg Lys Arg Cys Leu Phe Gly Gly Gln Glu
 20 25 30
 Pro Ala Pro Lys Glu Gln Pro Pro Leu Gln Pro Pro Gln Gln Ser
 35 40 45
 Ile Arg Val Lys Glu Glu Gln Tyr Leu Gly His Glu Gly Pro Gly Gly
 50 55 60
 Ala Val Ser Thr Ser Gln Pro Val Glu Leu Pro Pro Pro Ser Ser Leu
 65 70 75 80
 Ala Leu Leu Asn Ser Val Val Tyr Gly Pro Glu Arg Thr Ser Ala Ala
 85 90 95
 Met Leu Ser Gln Gln Val Ala Ser Val Lys Trp Pro Asn Ser Val Met
 100 105 110
 Ala Pro Gly Arg Gly Pro Glu Arg Gly Gly Gly Gly Val Ser Asp
 115 120 125
 Ser Ser Trp Gln Gln Gln Pro Gly Gln Pro Pro Pro His Ser Thr Trp
 130 135 140
 Asn Cys His Ser Leu Ser Leu Tyr Ser Ala Thr Lys Gly Ser Pro His
 145 150 155 160
 Pro Gly Val Gly Val Pro Thr Tyr Tyr Asn His Pro Glu Ala Leu Lys
 165 170 175
 Arg Glu Lys Ala Gly Gly Pro Gln Leu Asp Arg Tyr Val Arg Pro Met
 180 185 190
 Met Pro Gln Lys Val Gln Leu Glu Val Gly Arg Pro Gln Ala Pro Leu
 195 200 205
 Asn Ser Phe His Ala Ala Lys Lys Pro Pro Asn Gln Ser Leu Pro Leu
 210 215 220
 Gln Pro Phe Gln Leu Ala Phe Gly His Gln Val Asn Arg Gln Val Phe
 225 230 235 240
 Arg Gln Gly Pro Pro Pro Asn Pro Val Ala Ala Phe Pro Pro Gln
 245 250 255
 Lys Gln Gln Gln Gln Gln Gln Pro Gln Gln Gln Gln Gln Gln Gln
 260 265 270
 Ala Ala Leu Pro Gln Met Pro Leu Phe Glu Asn Phe Tyr Ser Met Pro
 275 280 285
 Gln Gln Pro Ser Gln Gln Pro Gln Asp Phe Gly Leu Gln Pro Ala Gly
 290 295 300
 Pro Leu Gly Gln Ser His Leu Ala His His Ser Met Ala Pro Tyr Pro
 305 310 315 320
 Phe Pro Pro Asn Pro Asp Met Asn Pro Glu Leu Arg Lys Ala Leu Leu
 325 330 335
 Gln Asp Ser Ala Pro Gln Pro Ala Leu Pro Gln Val Gln Ile Pro Phe
 340 345 350
 Pro Arg Arg Ser Arg Arg Leu Ser Lys Glu Gly Ile Leu Pro Pro Ser
 355 360 365
 Ala Leu Asp Gly Ala Gly Thr Gln Pro Gly Gln Glu Ala Thr Gly Asn
 370 375 380
 Leu Phe Leu His His Trp Pro Leu Gln Gln Pro Pro Pro Gly Ser Leu
 385 390 395 400
 Gly Gln Pro His Pro Glu Ala Leu Gly Phe Pro Leu Glu Leu Arg Glu
 405 410 415
 Ser Gln Leu Leu Pro Asp Gly Glu Arg Leu Ala Pro Asn Gly Arg Glu
 420 425 430
 Arg Glu Ala Pro Ala Met Gly Ser Glu Glu Gly Met Arg Ala Val Ser
 435 440 445
 Thr Gly Asp Cys Gly Gln Val Leu Arg Gly Gly Val Ile Gln Ser Thr
 450 455 460
 Arg Arg Arg Arg Ala Ser Gln Glu Ala Asn Leu Leu Thr Leu Ala
 465 470 475 480
 Gln Lys Ala Val Glu Leu Ala Ser Leu Gln Asn Ala Lys Asp Gly Ser
 485 490 495
 Gly Ser Glu Glu Lys Arg Lys Ser Val Leu Ala Ser Thr Thr Lys Cys
 500 505 510
 Gly Val Glu Phe Ser Glu Pro Ser Leu Ala Thr Lys Arg Ala Arg Glu
 515 520 525
 Asp Ser Gly Met Val Pro Leu Ile Ile Pro Val Ser Val Pro Val Arg
 530 535 540
 Thr Val Asp Pro Thr Glu Ala Ala Gln Ala Gly Gly Leu Asp Glu Asp
 545 550 555 560
 Gly Lys Gly Leu Glu Gln Asn Pro Ala Glu His Lys Pro Ser Val Ile
 565 570 575
 Val Thr Arg Arg Arg Ser Thr Arg Ile Pro Gly Thr Asp Ala Gln Ala
 580 585 590
 Gln Ala Glu Asp Met Asn Val Lys Leu Glu Gly Glu Pro Ser Val Arg


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      595      600      605
Lys Pro Lys Gln Arg Pro Arg Pro Glu Pro Leu Ile Ile Pro Thr Lys
  610      615      620
Ala Gly Thr Phe Ile Ala Pro Pro Val Tyr Ser Asn Ile Thr Pro Tyr
  625      630      635      640
Gln Ser His Leu Arg Ser Pro Val Arg Leu Ala Asp His Pro Ser Glu
      645      650      655
Arg Ser Phe Glu Leu Pro Pro Tyr Thr Pro Pro Pro Ile Leu Ser Pro
      660      665      670
Val Arg Glu Gly Ser Gly Leu Tyr Phe Asn Ala Ile Ile Ser Thr Ser
      675      680      685
Thr Ile Pro Ala Pro Pro Pro Ile Thr Pro Lys Ser Ala His Arg Thr
      690      695      700
Leu Leu Arg Thr Asn Ser Ala Glu Val Thr Pro Pro Val Leu Ser Val
  705      710      715      720
Met Gly Glu Ala Thr Pro Val Ser Ile Glu Pro Arg Ile Asn Val Gly
      725      730      735
Ser Arg Phe Gln Ala Glu Ile Pro Leu Met Arg Asp Arg Ala Leu Ala
      740      745      750
Ala Ala Asp Pro His Lys Ala Asp Leu Val Trp Gln Pro Trp Glu Asp
      755      760      765
Leu Glu Ser Ser Arg Glu Lys Gln Arg Gln Val Glu Asp Leu Leu Thr
      770      775      780
Ala Ala Cys Ser Ser Ile Phe Pro Gly Ala Gly Thr Asn Gln Glu Leu
  785      790      795      800
Ala Leu His Cys Leu His Glu Ser Arg Gly Asp Ile Leu Glu Thr Leu
      805      810      815
Asn Lys Leu Leu Leu Lys Lys Pro Leu Arg Pro His Asn His Pro Leu
      820      825      830
Ala Thr Tyr His Tyr Thr Gly Ser Asp Gln Trp Lys Met Ala Glu Arg
      835      840      845
Lys Leu Phe Asn Lys Gly Ile Ala Ile Tyr Lys Lys Asp Phe Phe Leu
      850      855      860
Val Gln Lys Leu Ile Gln Thr Lys Thr Val Ala Gln Cys Val Glu Phe
  865      870      875      880
Tyr Tyr Thr Tyr Lys Lys Gln Val Lys Ile Gly Arg Asn Gly Thr Leu
      885      890      895
Thr Phe Gly Asp Val Asp Thr Ser Asp Glu Lys Ser Ala Gln Glu Glu
      900      905      910
Val Glu Val Asp Ile Lys Thr Ser Gln Lys Phe Pro Arg Val Pro Leu
      915      920      925
Pro Arg Arg Glu Ser Pro Ser Glu Glu Arg Leu Glu Pro Lys Arg Glu
      930      935      940
Val Lys Glu Pro Arg Lys Glu Gly Glu Glu Glu Val Pro Glu Ile Gln
  945      950      955      960
Glu Lys Glu Glu Gln Glu Gly Arg Glu Arg Ser Arg Arg Ala Ala
      965      970      975
Ala Val Lys Ala Thr Gln Thr Leu Gln Ala Asn Glu Ser Ala Ser Asp
      980      985      990
Ile Leu Ile Leu Arg Ser His Glu Ser Asn Ala Pro Gly Ser Ala Gly
      995      1000      1005
Gly Gln Ala Ser Glu Lys Pro Arg Glu Gly Thr Gly Lys Ser Arg Arg
      1010      1015      1020
Ala Leu Pro Phe Ser Glu Lys Lys Lys Lys Lys Gln Lys Ala
  1025      1030      1035

```

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 849 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

```

Ile Arg His Glu Val Ser Phe Leu Trp Asn Thr Glu Ala Ala Cys Pro
  1      5      10      15
Ile Gln Thr Thr Thr Asp Thr Asp Gln Ala Cys Ser Ile Arg Asp Pro
      20      25      30
Asn Ser Gly Phe Val Phe Asn Leu Asn Pro Leu Asn Ser Ser Gln Gly
      35      40      45

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Tyr Asn Val Ser Gly Ile Gly Lys Ile Phe Met Phe Asn Val Cys Gly
 50 55 60
 Thr Met Pro Val Cys Gly Thr Ile Leu Gly Lys Pro Ala Ser Gly Cys
 65 70 75 80
 Glu Ala Glu Thr Gln Thr Glu Glu Leu Lys Asn Trp Lys Pro Ala Arg
 85 90 95
 Pro Val Gly Ile Glu Lys Ser Leu Gln Leu Ser Thr Glu Gly Phe Ile
 100 105 110
 Thr Leu Thr Tyr Lys Gly Pro Leu Ser Ala Lys Gly Thr Ala Asp Ala
 115 120 125
 Phe Ile Val Arg Phe Val Cys Asn Asp Asp Val Tyr Ser Gly Pro Leu
 130 135 140
 Lys Phe Leu His Gln Asp Ile Asp Ser Gly Gln Gly Ile Arg Asn Thr
 145 150 155 160
 Tyr Phe Glu Phe Glu Thr Ala Leu Ala Cys Val Pro Ser Pro Val Asp
 165 170 175
 Cys Gln Val Thr Asp Leu Ala Gly Asn Glu Tyr Asp Leu Thr Gly Leu
 180 185 190
 Ser Thr Val Arg Lys Pro Trp Thr Ala Val Asp Thr Ser Val Asp Gly
 195 200 205
 Arg Lys Arg Thr Phe Tyr Leu Ser Val Cys Asn Pro Leu Pro Tyr Ile
 210 215 220
 Pro Gly Cys Gln Gly Ser Ala Val Gly Ser Cys Leu Val Ser Glu Gly
 225 230 235 240
 Asn Ser Trp Asn Leu Gly Val Val Gln Met Ser Pro Gln Ala Ala Ala
 245 250 255
 Asn Gly Ser Leu Ser Ile Met Tyr Val Asn Gly Asp Lys Cys Gly Asn
 260 265 270
 Gln Arg Phe Ser Thr Arg Ile Thr Phe Glu Cys Ala Gln Ile Ser Gly
 275 280 285
 Ser Pro Ala Phe Gln Leu Gln Asp Gly Cys Glu Tyr Val Phe Ile Trp
 290 295 300
 Arg Thr Val Glu Ala Cys Pro Val Val Arg Val Glu Gly Asp Asn Cys
 305 310 315 320
 Glu Val Lys Asp Pro Arg His Gly Asn Leu Tyr Asp Leu Lys Pro Leu
 325 330 335
 Gly Leu Asn Asp Thr Ile Val Ser Ala Gly Glu Tyr Thr Tyr Tyr Phe
 340 345 350
 Arg Val Cys Gly Lys Leu Ser Ser Asp Val Cys Pro Thr Ser Asp Lys
 355 360 365
 Ser Lys Val Val Ser Ser Cys Gln Glu Lys Arg Glu Pro Gln Gly Phe
 370 375 380
 His Lys Val Ala Gly Leu Leu Thr Gln Lys Leu Thr Tyr Glu Asn Gly
 385 390 395 400
 Leu Leu Lys Met Asn Phe Thr Gly Gly Asp Thr Cys His Lys Val Tyr
 405 410 415
 Gln Arg Ser Thr Ala Ile Phe Phe Tyr Cys Asp Arg Gly Thr Gln Arg
 420 425 430
 Pro Val Phe Leu Lys Glu Thr Ser Asp Cys Ser Tyr Leu Phe Glu Trp
 435 440 445
 Arg Thr Gln Tyr Ala Cys Pro Pro Phe Asp Leu Thr Glu Cys Ser Phe
 450 455 460
 Lys Asp Gly Ala Gly Asn Ser Phe Asp Leu Ser Ser Leu Ser Arg Tyr
 465 470 475 480
 Ser Asp Asn Trp Glu Ala Ile Thr Gly Thr Gly Asp Pro Glu His Tyr
 485 490 495
 Leu Ile Asn Val Cys Lys Ser Leu Ala Pro Gln Ala Gly Thr Glu Pro
 500 505 510
 Cys Pro Pro Glu Ala Ala Ala Cys Leu Leu Gly Gly Ser Lys Pro Val
 515 520 525
 Asn Leu Gly Arg Val Arg Asp Gly Pro Gln Trp Arg Asp Gly Ile Ile
 530 535 540
 Val Leu Lys Tyr Val Asp Gly Asp Leu Cys Pro Asp Gly Ile Arg Lys
 545 550 555 560
 Lys Ser Thr Thr Ile Arg Phe Thr Cys Ser Glu Ser Gln Val Asn Ser
 565 570 575
 Arg Pro Met Phe Ile Ser Ala Val Glu Asp Cys Glu Tyr Thr Phe Ala
 580 585 590
 Trp Pro Thr Ala Thr Ala Cys Pro Met Lys Ser Asn Glu His Asp Asp
 595 600 605
 Cys Gln Val Thr Asn Pro Ser Thr Gly His Leu Phe Asp Leu Ser Ser
 610 615 620
 Leu Ser Gly Arg Ala Gly Phe Thr Ala Ala Tyr Ser Glu Lys Gly Leu

```

625          630          635          640
Val Tyr Met Ser Ile Cys Gly Glu Asn Glu Asn Cys Pro Pro Gly Val
645          650          655
Gly Ala Cys Phe Gly Gln Thr Arg Ile Ser Val Gly Lys Ala Asn Lys
660          665          670
Arg Leu Arg Tyr Val Asp Gln Val Leu Gln Leu Val Tyr Lys Asp Gly
675          680          685
Ser Pro Cys Pro Ser Lys Ser Gly Leu Ser Tyr Lys Ser Val Ile Ser
690          695          700
Phe Val Cys Arg Pro Glu Ala Gly Pro Thr Asn Arg Pro Met Leu Ile
705          710          715          720
Ser Leu Asp Lys Gln Thr Cys Thr Leu Phe Phe Ser Trp His Thr Pro
725          730          735
Leu Ala Cys Glu Gln Ala Thr Glu Cys Ser Val Arg Asn Gly Ser Ser
740          745          750
Ile Val Asp Leu Ser Pro Leu Ile His Arg Thr Gly Gly Tyr Glu Ala
755          760          765
Tyr Asp Glu Ser Glu Asp Asp Ala Ser Asp Thr Asn Pro Asp Phe Tyr
770          775          780
Ile Asn Ile Cys Gln Pro Leu Asn Pro Met His Gly Val Pro Cys Pro
785          790          795          800
Ala Gly Ala Ala Val Cys Lys Val Pro Ile Asp Gly Pro Pro Ile Asp
805          810          815
Ile Gly Arg Val Ala Gly Pro Pro Ile Leu Asn Pro Ile Ala Asn Glu
820          825          830
Ile Tyr Leu Asn Phe Glu Ser Ser Thr Pro Cys Gln Glu Phe Ser Cys
835          840          845
Lys

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(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 852 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

```

Met Ala Arg Leu Ser Arg Pro Glu Arg Pro Asp Leu Val Phe Glu Glu
1          5          10          15
Glu Asp Leu Pro Tyr Glu Glu Glu Ile Met Arg Asn Gln Phe Ser Val
20          25          30
Lys Cys Trp Leu His Tyr Ile Glu Phe Lys Gln Gly Ala Pro Lys Pro
35          40          45
Arg Leu Asn Gln Leu Tyr Glu Arg Ala Leu Lys Leu Leu Pro Cys Ser
50          55          60
Tyr Lys Leu Trp Tyr Arg Tyr Leu Lys Ala Arg Arg Ala Gln Val Lys
65          70          75          80
His Arg Cys Val Thr Asp Pro Ala Tyr Glu Asp Val Asn Asn Cys His
85          90          95
Glu Arg Ala Phe Val Phe Met His Lys Met Pro Arg Leu Trp Leu Asp
100          105          110
Tyr Cys Gln Phe Leu Met Asp Gln Gly Arg Val Thr His Thr Arg Arg
115          120          125
Thr Phe Asp Arg Ala Leu Arg Ala Leu Pro Ile Thr Gln His Ser Arg
130          135          140
Ile Trp Pro Leu Tyr Leu Arg Phe Leu Arg Ser His Pro Leu Pro Glu
145          150          155          160
Thr Ala Val Arg Gly Tyr Arg Arg Phe Leu Lys Leu Ser Pro Glu Ser
165          170          175
Ala Glu Glu Tyr Ile Glu Tyr Leu Lys Ser Ser Asp Arg Leu Asp Glu
180          185          190
Ala Ala Gln Arg Leu Ala Thr Val Asn Asp Glu Arg Phe Val Ser
195          200          205
Lys Ala Gly Lys Ser Asn Tyr Gln Leu Trp His Glu Leu Cys Asp Leu
210          215          220
Ile Ser Gln Asn Pro Asp Lys Val Gln Ser Leu Asn Val Asp Ala Ile
225          230          235          240
Ile Arg Gly Gly Leu Thr Arg Phe Thr Asp Gln Leu Gly Lys Leu Trp
245          250          255

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Cys Ser Leu Ala Asp Tyr Tyr Ile Arg Ser Gly His Phe Glu Lys Ala
 260 265 270
 Arg Asp Val Tyr Glu Glu Ala Ile Arg Thr Val Met Thr Val Arg Asp
 275 280 285
 Phe Thr Gln Val Phe Asp Ser Tyr Ala Gln Phe Glu Glu Ser Met Ile
 290 295 300
 Ala Ala Lys Met Glu Thr Ala Ser Glu Leu Gly Arg Glu Glu Glu Asp
 305 310 315 320
 Asp Val Asp Leu Glu Leu Arg Leu Ala Arg Phe Glu Gln Leu Ile Ser
 325 330 335
 Arg Arg Pro Leu Leu Leu Asn Ser Val Leu Leu Arg Gln Asn Pro His
 340 345 350
 His Val His Glu Trp His Lys Arg Val Ala Leu His Gln Gly Arg Pro
 355 360 365
 Arg Glu Ile Ile Asn Thr Tyr Thr Glu Ala Val Gln Thr Val Asp Pro
 370 375 380
 Phe Lys Ala Thr Gly Lys Pro His Thr Leu Trp Val Ala Phe Ala Lys
 385 390 395 400
 Phe Tyr Glu Asp Asn Gly Gln Leu Asp Asp Ala Arg Val Ile Leu Glu
 405 410 415
 Lys Ala Thr Lys Val Asn Phe Lys Gln Val Asp Asp Leu Ala Ser Val
 420 425 430
 Trp Cys Gln Cys Gly Glu Leu Glu Leu Arg His Glu Asn Tyr Asp Glu
 435 440 445
 Ala Leu Arg Leu Leu Arg Lys Ala Thr Ala Leu Pro Ala Arg Arg Ala
 450 455 460
 Glu Tyr Phe Asp Gly Ser Glu Pro Val Gln Asn Arg Val Tyr Lys Ser
 465 470 475 480
 Leu Lys Val Trp Ser Met Leu Ala Asp Leu Glu Glu Ser Leu Gly Thr
 485 490 495
 Phe Gln Ser Thr Lys Ala Val Tyr Asp Arg Ile Leu Asp Leu Arg Ile
 500 505 510
 Ala Thr Pro Gln Ile Val Ile Asn Tyr Ala Met Phe Leu Glu Glu His
 515 520 525
 Lys Tyr Phe Glu Glu Ser Phe Lys Ala Tyr Glu Arg Gly Ile Ser Leu
 530 535 540
 Phe Lys Trp Pro Asn Val Ser Asp Ile Trp Ser Thr Tyr Leu Thr Lys
 545 550 555 560
 Phe Ile Ala Arg Tyr Gly Gly Arg Lys Leu Glu Arg Ala Arg Asp Leu
 565 570 575
 Phe Glu Gln Ala Leu Asp Gly Cys Pro Pro Lys Tyr Ala Lys Thr Leu
 580 585 590
 Tyr Leu Leu Tyr Ala Gln Leu Glu Glu Trp Gly Leu Ala Arg His
 595 600 605
 Ala Met Ala Val Tyr Glu Arg Ala Thr Arg Ala Val Glu Pro Ala Gln
 610 615 620
 Gln Tyr Asp Met Phe Asn Ile Tyr Ile Lys Arg Ala Ala Glu Ile Tyr
 625 630 635 640
 Gly Val Thr His Thr Arg Gly Ile Tyr Gln Lys Ala Ile Glu Val Leu
 645 650 655
 Ser Asp Glu His Ala Arg Glu Met Cys Leu Arg Phe Ala Asp Met Glu
 660 665 670
 Cys Lys Leu Gly Glu Ile Asp Arg Ala Arg Ala Ile Tyr Ser Phe Cys
 675 680 685
 Ser Gln Ile Cys Asp Pro Arg Thr Thr Gly Ala Phe Trp Gln Thr Trp
 690 695 700
 Lys Asp Phe Glu Val Arg His Gly Asn Glu Asp Thr Ile Lys Glu Met
 705 710 715 720
 Leu Arg Ile Arg Arg Ser Val Gln Ala Thr Tyr Asn Thr Gln Val Asn
 725 730 735
 Phe Met Ala Ser Gln Met Leu Lys Val Ser Gly Ser Ala Thr Gly Thr
 740 745 750
 Val Ser Asp Leu Ala Pro Gly Gln Ser Gly Met Asp Asp Met Lys Leu
 755 760 765
 Leu Glu Gln Arg Ala Glu Gln Leu Ala Ala Glu Ala Glu Arg Asp Gln
 770 775 780
 Pro Leu Arg Ala Gln Ser Lys Ile Leu Phe Val Arg Ser Asp Ala Ser
 785 790 795 800
 Arg Glu Glu Leu Ala Glu Leu Ala Gln Val Asn Pro Glu Glu Ile
 805 810 815
 Gln Leu Gly Glu Asp Glu Asp Glu Met Asp Leu Glu Pro Asn
 820 825 830
 Glu Val Arg Leu Glu Gln Gln Ser Val Pro Ala Ala Val Phe Gly Ser

835
Leu Lys Glu Asp
850

840

845

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 693 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

```

Met Phe Ser Ala Leu Lys Lys Leu Val Gly Ser Asp Gln Ala Pro Gly
 1           5           10           15
Arg Asp Lys Asn Ile Pro Ala Gly Leu Gln Ser Met Asn Gln Ala Leu
 20           25           30
Gln Arg Arg Phe Ala Lys Gly Val Gln Tyr Asn Met Lys Ile Val Ile
 35           40           45
Arg Gly Asp Arg Asn Thr Gly Lys Thr Ala Leu Trp His Arg Leu Gln
 50           55           60
Gly Arg Pro Phe Val Glu Glu Tyr Ile Pro Thr Gln Glu Ile Gln Val
 65           70           75           80
Thr Ser Ile His Trp Ser Tyr Lys Thr Thr Asp Asp Ile Val Lys Val
 85           90           95
Glu Val Trp Asp Val Val Asp Lys Gly Lys Cys Lys Lys Arg Gly Asp
100           105           110
Gly Leu Lys Met Glu Asn Asp Pro Gln Glu Xaa Glu Ser Glu Met Ala
115           120           125
Leu Asp Ala Glu Phe Leu Asp Val Tyr Lys Asn Cys Asn Gly Val Val
130           135           140
Met Met Phe Asp Ile Thr Lys Gln Trp Thr Phe Asn Tyr Ile Leu Arg
145           150           155           160
Glu Leu Pro Lys Val Pro Thr His Val Pro Val Cys Val Leu Gly Asn
165           170           175
Tyr Arg Asp Met Gly Glu His Arg Val Ile Leu Pro Asp Asp Val Arg
180           185           190
Asp Phe Ile Asp Asn Leu Asp Arg Pro Pro Gly Ser Ser Tyr Phe Arg
195           200           205
Tyr Ala Glu Ser Ser Met Lys Asn Ser Phe Gly Leu Lys Tyr Leu His
210           215           220
Lys Phe Phe Asn Ile Pro Phe Leu Gln Leu Gln Arg Glu Thr Leu Leu
225           230           235           240
Arg Gln Leu Glu Thr Asn Gln Leu Asp Met Asp Ala Thr Leu Glu Glu
245           250           255
Leu Ser Val Gln Gln Glu Thr Glu Asp Gln Asn Tyr Gly Ile Phe Leu
260           265           270
Glu Met Met Glu Ala Arg Ser Arg Gly His Ala Ser Pro Leu Ala Ala
275           280           285
Asn Gly Gln Ser Pro Ser Pro Gly Ser Gln Ser Pro Val Leu Pro Ala
290           295           300
Pro Ala Val Ser Thr Gly Ser Ser Ser Pro Gly Thr Pro Gln Pro Ala
305           310           315           320
Pro Gln Leu Pro Leu Asn Ala Ala Pro Pro Ser Ser Val Pro Pro Val
325           330           335
Pro Pro Ser Glu Ala Leu Pro Pro Pro Ala Cys Pro Ser Ala Pro Ala
340           345           350
Pro Arg Arg Ser Ile Ile Ser Arg Leu Phe Gly Thr Ser Pro Ala Thr
355           360           365
Glu Ala Ala Pro Pro Pro Pro Glu Pro Val Pro Ala Ala Gln Gly Pro
370           375           380
Ala Thr Val Gln Ser Val Glu Asp Phe Val Pro Asp Asp Arg Leu Asp
385           390           395           400
Arg Ser Phe Leu Glu Asp Thr Thr Pro Ala Arg Asp Glu Lys Lys Val
405           410           415
Gly Ala Lys Ala Ala Gln Gln Asp Ser Asp Ser Asp Gly Glu Ala Leu
420           425           430
Gly Gly Asn Pro Met Val Ala Gly Phe Gln Asp Asp Val Asp Leu Glu
435           440           445
Asp Gln Pro Arg Gly Ser Pro Pro Leu Pro Ala Gly Pro Val Pro Ser
450           455           460

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Gln Asp Ile Thr Leu Ser Ser Glu Glu Glu Ala Glu Val Ala Ala Pro
 465 470 475 480
 Thr Lys Gly Pro Ala Pro Ala Pro Gln Gln Cys Ser Glu Pro Glu Thr
 485 490 495
 Lys Trp Ser Ser Ile Pro Ala Ser Lys Pro Arg Arg Gly Thr Ala Pro
 500 505 510
 Thr Arg Thr Ala Ala Pro Pro Trp Pro Gly Gly Val Ser Val Arg Thr
 515 520 525
 Gly Pro Glu Lys Arg Ser Ser Thr Arg Pro Pro Ala Glu Met Glu Pro
 530 535 540
 Gly Lys Gly Glu Gln Ala Ser Ser Ser Glu Ser Asp Pro Glu Gly Pro
 545 550 555 560
 Ile Ala Ala Gln Met Leu Ser Phe Val Met Asp Asp Pro Asp Phe Glu
 565 570 575
 Ser Glu Gly Ser Asp Thr Gln Arg Arg Ala Asp Asp Phe Pro Val Arg
 580 585 590
 Asp Asp Pro Ser Asp Val Thr Asp Glu Asp Glu Gly Pro Ala Glu Pro
 595 600 605
 Pro Pro Pro Pro Lys Leu Pro Leu Pro Ala Phe Arg Leu Lys Asn Asp
 610 615 620
 Ser Asp Leu Phe Gly Leu Gly Leu Glu Glu Ala Gly Pro Lys Glu Ser
 625 630 635 640
 Ser Glu Glu Gly Lys Glu Gly Lys Thr Pro Ser Lys Glu Lys Lys Lys
 645 650 655
 Lys Thr Lys Ser Phe Ser Arg Val Leu Leu Glu Arg Pro Arg Ala His
 660 665 670
 Arg Phe Ser Thr Arg Val Gly Tyr Gln Val Ser Val Pro Asn Ser Pro
 675 680 685
 Tyr Ser Glu Ser Tyr
 690